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OM protein - protein search, using sw model

Run on: July 3, 2001, 10:00:55 ; Search time 21.69 Seconds
(without alignments)
8.359 Million cell updates/sec

Title: US-09-214-836-1

Sequence: 1 KTWGQYNAV 9

Scoring table: BLOSUM62
Gap 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	91.4	9	1	US-08-787-547-61
2	53	91.4	9	2	US-08-417-174-46
3	53	91.4	9	2	US-08-902-516-29
4	53	91.4	9	2	US-09-036-582-26
5	53	91.4	10	2	US-08-417-174-47
6	53	91.4	661	2	US-08-417-174-121
7	53	91.4	668	1	US-07-891-942G-6
8	50	86.2	661	2	US-08-417-174-27
9	50	86.2	661	2	US-08-231-565A-27
10	50	86.2	661	2	US-09-007-961-27
11	48	82.8	9	2	US-08-417-174-71
12	48	82.8	9	2	US-08-417-174-72
13	48	82.8	9	2	US-08-417-174-73
14	48	82.8	9	2	US-08-417-174-74
15	48	82.8	9	2	US-08-417-174-75
16	47	81.0	9	2	US-08-417-174-68
17	47	81.0	9	2	US-08-417-174-69
18	47	81.0	9	2	US-08-417-174-70
19	44	75.9	9	2	US-08-417-174-76
20	43	74.1	9	2	US-08-417-174-77
21	43	74.1	9	2	US-08-417-174-78
22	43	74.1	9	2	US-08-417-174-79
23	43	74.1	9	2	US-08-417-174-80
24	43	74.1	9	2	US-08-417-174-81
25	43	74.1	9	2	US-08-417-174-82
26	40	69.0	72	1	US-08-482-282B-6
27	40	69.0	72	1	US-08-486-036A-6

28	40	69.0	72	5	PCT-US96-09848-6	Sequence 6, Appl
29	40	69.0	401	5	PCT-US96-09848-31	Sequence 31, Appl
30	40	69.0	407	5	PCT-US96-09848-15	Sequence 15, Appl
31	39	67.2	585	1	US-08-212-188-4	Sequence 4, Appl
32	39	67.2	585	3	US-08-970-725-4	Sequence 4, Appl
33	39	67.2	585	5	PCT-US95-02708-4	Sequence 4, Appl
34	37	63.8	12	1	US-08-439-817-205	Sequence 205, App
35	37	63.8	20	1	US-08-241-054-85	Sequence 85, Appl
36	37	63.8	20	1	US-08-241-054-91	Sequence 91, Appl
37	37	63.8	20	1	US-08-390-156A-40	Sequence 40, Appl
38	37	63.8	20	1	US-08-390-156A-43	Sequence 43, Appl
39	37	63.8	20	1	US-08-439-817-65	Sequence 65, Appl
40	37	63.8	20	1	US-08-439-817-71	Sequence 71, Appl
41	37	63.8	20	1	US-08-485-508-85	Sequence 85, Appl
42	37	63.8	20	1	US-08-485-508-91	Sequence 91, Appl
43	37	63.8	191	1	US-08-044-621D-35	Sequence 35, Appl
44	37	63.8	191	1	US-08-709-912-11	Sequence 11, Appl
45	37	63.8	191	2	US-09-047-370-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-787-547-61
Sequence 61, Application US/08787547
Patent No. 5783567
GENERAL INFORMATION:
APPLICANT: Hedley, Mary Lynne
APPLICANT: Curley, Joanne M.
APPLICANT: Langer, Robert S.
TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
TITLE OF INVENTION: OF NUCLEIC ACID
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/787,547
FILING DATE: 22-JAN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-787-547-61
Query Match 91.4%; Score 53; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYWAY 9
11111111
DB 1 KTWGQYWAY 9

RESULT 2

US-08-417-174-46
; Sequence 46, Application US/08417174
; Patent No. 5844075
; GENERAL INFORMATION:
; APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG,
; APPLICANT: STEVEN A.
; TITLE OF INVENTION: MELANOMA ANTIGENS AND
; TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
; NUMBER OF INVENTIONS: METHODS
; NUMBER OF SEQUENCES: 126
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/417,174
; FILING DATE: 05-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,565
; FILING DATE: 22-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CAROL M. GRUPPI
; REGISTRATION NUMBER: 37,341
; REFERENCE/DOCKET NUMBER: 2026-4124US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: amino acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-417-174-46

Query Match 91.4%; Score 53; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYWAY 9
11111111
DB 1 KTWGQYWAY 9

RESULT 3
US-08-902-516-29
; Sequence 29, Application US/08902516
; Patent No. 5891432
; GENERAL INFORMATION:
; APPLICANT: SOO HOO, WILLIAM
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
; TITLE OF INVENTION: COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
; TITLE OF INVENTION: RESPONSE USING SAME
; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,516
; FILING DATE: 29-JUL-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-1M 2442
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)535-9001
; TELEFAX: (619)535-8949
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-902-516-29

Query Match 91.4%; Score 53; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYWAY 9
11111111
DB 1 KTWGQYWAY 9

RESULT 4
US-09-036-582-26
; Sequence 26, Application US/09036582A
; Patent No. 5965381
; GENERAL INFORMATION:
; APPLICANT: van der Bruggen, Pierre
; TITLE OF INVENTION: DELIVERY OF PROTEINS INTO EUKARYOTIC CELLS
; FILE REFERENCE: 11154
; CURRENT APPLICATION NUMBER: US/09/036,582A
; CURRENT FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 26
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human gp100pmell17 peptide
US-09-036-582-26

Query Match 91.4%; Score 53; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYWAY 9
11111111
DB 1 KTWGQYWAY 9

RESULT 5
US-08-417-174-47

Sequence 47, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-47

Query Match 91.4%; Score 53; DB 2; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.012;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTWGQYNAV 9
Db 1 KTWGQYNAV 9

RESULT 6
US-08-417-174-121
Sequence 121, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 661
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Protein
US-08-417-174-121

Query Match 91.4%; Score 53; DB 2; Length 661;
Best Local Similarity 88.9%; Pred. No. 0.75;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTWGQYNAV 9
Db 154 KTWGQYNAV 162

RESULT 7
US-07-891-942G-6
Sequence 6, Application US/07891942G
Patent No. 5679511
GENERAL INFORMATION:
APPLICANT: Kwon, Byoung Se
TITLE OF INVENTION: cDNA CLONES FOR HUMAN TYROSINASE AND FOR
A REGULATORY PROTEIN IN THE MELANIN PROTEIN PATHWAY
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christopher A. Michaels, Barnard, Brown &
STREET: 306 East State Street, Suite 220
CITY: Ithaca
STATE: NY
COUNTRY: USA
ZIP: 14850
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,942G
FILING DATE: 01-JUN-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/915,753
FILING DATE: 06-OCT-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/362,847
FILING DATE: 07-JUN-1989
ATTORNEY/AGENT INFORMATION:
NAME: Michaels, Christopher A

REGISTRATION NUMBER: 34,390
REFERENCE/DOCKET NUMBER: INDI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 607-273-1711
TELEFAX: 607-273-2609
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 668 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PUBLICATION INFORMATION:
AUTHORS: Kwon, Byoung Se
AUTHORS: Chintamani, Chaya
AUTHORS: Kozak, Christine A
AUTHORS: Copeland, Neal G
AUTHORS: Gilbert, Debra J
AUTHORS: Jenkins, Nancy
AUTHORS: Barton, David
AUTHORS: Francke, Uta
AUTHORS: Kobayashi, Yvonne
AUTHORS: Kim, Kack K
TITLE: A melanocyte-specific gene, Pmel 17, maps
TITLE: near the silver coat color locus on mouse
TITLE: chromosome 10 and is in a syntenic region on human
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
VOLUME: 88
PAGES: 9228-9232
DATE: October 1991
RELEVANT RESIDUES IN SEQ ID NO: 6: FROM 1 TO 668
US-07-891-9426-6

Query Match
Best Local Similarity 91.4%; Score 53; DB 1; Length 668;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYMW 9
DB 154 KTWGQYMW 162

RESULT 8
US-08-417-174-27
Sequence 27, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAKAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPE
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 661
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: Protein
US-08-417-174-27

Query Match
Best Local Similarity 86.2%; Score 50; DB 2; Length 661;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KTWGQYMW 7
DB 154 KTWGQYMW 160

RESULT 9
US-08-231-565A-27
Sequence 27, Application US/08231565A
Patent No. 5874560
GENERAL INFORMATION:
APPLICANT: KAKAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565A
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPE
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 661
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: Protein
US-08-231-565A-27

Query Match 86.2%; Score 50; DB 2; Length 661;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTMGOYW 7
1111111
Db 154 KTMGOYW 160

RESULT 10
US-09-007-961-27
; Sequence 27, Application US/09007961
; Patent No. 5994523
; GENERAL INFORMATION:
; APPLICANT: KAKAKAMI, YUTAKA; ROSENBERG,
; APPLICANT: STEVEN A.
; TITLE OF INVENTION: MELANOMA ANTIGENS AND
; TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/007,961
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/231,565
; FILING DATE: 22-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: CAROL M. GRUPE
; REGISTRATION NUMBER: 37,341
; REFERENCE/DOCKET NUMBER: 2026-4124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 661
; TYPE: amino acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Protein
US-09-007-961-27

Query Match 86.2%; Score 50; DB 2; Length 661;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTMGOYW 7
1111111
Db 154 KTMGOYW 160

RESULT 11
US-08-417-174-71
; Sequence 71, Application US/08417174
; Patent No. 5844075
; GENERAL INFORMATION:
; APPLICANT: KAKAKAMI, YUTAKA; ROSENBERG,
; APPLICANT: STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPE
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-71

Query Match 82.8%; Score 48; DB 2; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.4e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TWGOYMW 9
1111111
Db 2 TWGOYMW 9

RESULT 12
US-08-417-174-72
; Sequence 72, Application US/08417174
; Patent No. 5844075
; GENERAL INFORMATION:
; APPLICANT: KAKAKAMI, YUTAKA; ROSENBERG,
; APPLICANT: STEVEN A.
; TITLE OF INVENTION: MELANOMA ANTIGENS AND
; TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 126
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-72

Query Match 82.8%; Score 48; DB 2; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.4e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TWGQYNAV 9
DB 2 TWGQYMOV 9

RESULT 13
US-08-417-174-73
Sequence 73, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 73:

SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-73

Query Match 82.8%; Score 48; DB 2; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.4e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TWGQYNAV 9
DB 2 TWGQYMOV 9

RESULT 14
US-08-417-174-74
Sequence 74, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-74

Query Match 82.8%; Score 48; DB 2; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.4e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TWGQYNAV 9
DB 2 TWGQYMOV 9

RESULT 15
US-08-417-174-75
Sequence 75, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-75

Query Match 82.8%; Score 48; DB 2; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.4e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TWGQYWAY 9
Db 2 TWGQYWAY 9

RESULT 16
US-08-417-174-68
Sequence 68, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE

CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-68

Query Match 81.0%; Score 47; DB 2; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.4e+05;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTWGQYWAY 9
Db 1 KTWGQYWAY 9

RESULT 17
US-08-417-174-69
Sequence 69, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-69

Query Match 81.0%; Score 47; DB 2; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.4e+05;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTWGQYWAY 9
| | | | | | |
DB 1 KMWGQYWAY 9

RESULT 18
US-08-417-174-70
Sequence 70, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A. MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-70

Query Match 81.0%; Score 47; DB 2; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.4e+05;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTWGQYWAY 9
| | | | | | |
DB 1 KTWGQYWAY 9

RESULT 19
US-08-417-174-76
Sequence 76, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A. MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-76

Query Match 75.9%; Score 44; DB 2; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.4e+05;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTWGQYWAY 9
| | | | | | |
DB 1 KTWGQYWAY 9

RESULT 20
US-08-417-174-77
Sequence 77, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:

APPLICANT: KAKAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: Peptide
US-08-417-174-77

Query Match 74.1%; Score 43; DB 2; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.4e+05;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTWGOYNAV 9
||:|||||
Db 1 KTFGOYMOV 9

RESULT 21
US-08-417-174-78
Sequence 78, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAKAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: Peptide
US-08-417-174-78

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: Peptide
US-08-417-174-78

Query Match 74.1%; Score 43; DB 2; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.4e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WGOYNAV 9
||:|||||
Db 3 WGOYMOV 9

RESULT 22
US-08-417-174-79
Sequence 79, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAKAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: Peptide
US-08-417-174-78

TELEX: 421792
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: amino acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-417-174-79

Query Match 74.1%; Score 43; DB 2; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.4e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WGOYMAV 9
Db 3 WGOYMOV 9

RESULT 23
US-08-417-174-80
; Sequence 80, Application US/08417174
; Patent No. 5844075
; GENERAL INFORMATION:
; APPLICANT: KAKAKAMI, YUTAKA; ROSENBERG,
; APPLICANT: STEVEN A.
; TITLE OF INVENTION: MELANOMA ANTIGENS AND
; TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
; NUMBER OF SEQUENCES: 126
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/417,174
; FILING DATE: 05-APR-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,565
; FILING DATE: 22-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CAROL M. GRUPPI
; REGISTRATION NUMBER: 37,341
; REFERENCE/DOCKET NUMBER: 2026-4124US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 751-6849
; TELEFAX: (212) 751-6800
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: amino acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-417-174-80

Query Match 74.1%; Score 43; DB 2; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.4e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WGOYMAV 9

Db 3 WGOYMOV 9

RESULT 24
US-08-417-174-81
; Sequence 81, Application US/08417174
; Patent No. 5844075
; GENERAL INFORMATION:
; APPLICANT: KAKAKAMI, YUTAKA; ROSENBERG,
; APPLICANT: STEVEN A.
; TITLE OF INVENTION: MELANOMA ANTIGENS AND
; TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
; NUMBER OF SEQUENCES: 126
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/417,174
; FILING DATE: 05-APR-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,565
; FILING DATE: 22-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CAROL M. GRUPPI
; REGISTRATION NUMBER: 37,341
; REFERENCE/DOCKET NUMBER: 2026-4124US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 751-6849
; TELEFAX: (212) 751-6800
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: amino acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-417-174-81

Query Match 74.1%; Score 43; DB 2; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.4e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WGOYMAV 9
Db 3 WGOYMOV 9

RESULT 25
US-08-417-174-82
; Sequence 82, Application US/08417174
; Patent No. 5844075
; GENERAL INFORMATION:
; APPLICANT: KAKAKAMI, YUTAKA; ROSENBERG,
; APPLICANT: STEVEN A.
; TITLE OF INVENTION: MELANOMA ANTIGENS AND
; TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
; NUMBER OF SEQUENCES: 126
; CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-82

Query Match 74.1%; Score 43; DB 2; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.4e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 WGYWAV 9
|||
Db 3 WGYWAV 9

RESULT 26
US-08-482-282B-6
Sequence 6, Application US/08482282B
Patent No. 5792624
GENERAL INFORMATION:
APPLICANT: TRIPP, Cynthia A.
APPLICANT: Wisniewski, Nancy
APPLICANT: Gileve, Robert B.
APPLICANT: Frank, Glenn R.
TITLE OF INVENTION: NOVEL FILARIID NEMATODE CYSTEINE
TITLE OF INVENTION: PROTEASE PROTEIN, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEROP
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,282B

FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: 2618-33-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (970) 493-7272
TELEFAX: (970) 484-9505
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 72 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-282B-6

Query Match 69.0%; Score 40; DB 1; Length 72;
Best Local Similarity 55.6%; Pred. No. 7.5;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGYWAV 9
|||
Db 30 KTYGEYWI 38

RESULT 27
US-08-486-036A-6
Sequence 6, Application US/08486036A
Patent No. 5795768
GENERAL INFORMATION:
APPLICANT: TRIPP, Cynthia A.
APPLICANT: Wisniewski, Nancy
APPLICANT: Gileve, Robert B.
APPLICANT: Frank, Glenn R.
TITLE OF INVENTION: NOVEL FILARIID NEMATODE
TITLE OF INVENTION: CYSTEINE PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES AND USES THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,036A
FILING DATE: June 7, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-33
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 72 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-486-036A-6

Query Match 69.0%; Score 40; DB 1; Length 72;

Best Local Similarity 55.6%; Pred. No. 7.5;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYWAY 9
Db 30 KTYGEYWI 38

RESULT 28

PCT-US96-09848-6
; Sequence 6, Application PC/TUS9609848
; GENERAL INFORMATION:
; APPLICANT: Tripp, Cynthia A.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: NOVEL FILARIID NEMATODE CYSTEINE
; TITLE OF INVENTION: PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09848
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/486,036
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2618-33-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 72 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-09848-6

Query Match 69.0%; Score 40; DB 5; Length 72;
Best Local Similarity 55.6%; Pred. No. 7.5;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYWAY 9
Db 30 KTYGEYWI 38

RESULT 29

PCT-US96-09848-31
; Sequence 31, Application PC/TUS9609848
; GENERAL INFORMATION:
; APPLICANT: Tripp, Cynthia A.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: NOVEL FILARIID NEMATODE CYSTEINE
; TITLE OF INVENTION: PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500

CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09848
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,036
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-33-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-09848-31

Query Match 69.0%; Score 40; DB 5; Length 401;
Best Local Similarity 55.6%; Pred. No. 41;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYWAY 9
Db 359 KTYGEYWI 367

RESULT 30

PCT-US96-09848-15
; Sequence 15, Application PC/TUS9609848
; GENERAL INFORMATION:
; APPLICANT: Tripp, Cynthia A.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: NOVEL FILARIID NEMATODE CYSTEINE
; TITLE OF INVENTION: PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09848
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/486,036
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2618-33-PCT

TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 407 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-09848-15

Query Match 69.0%; Score 40; DB 5; Length 407;
Best Local Similarity 55.6%; Pred. No. 42;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 KTWGQYMAV 9
||:|:|:
Db 365 KTYGEYWI 373

Search completed: July 3, 2001, 10:22:35
Job time: 1300 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2001, 10:22:40 ; Search time 37.77 Seconds

(without alignments)
31.526 Million cell updates/sec

Title: US-09-214-836-1

Sequence: 1 KTWGQYMAV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP-organelle:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP_unclassified:*
13: SP-vertebrate:*
14: SP-virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	72.4	902	2	Q9S1E4
2	41	70.7	116	3	Q9UVZ4
3	41	70.7	458	5	O18533
4	40	69.0	276	1	O9Y9N5
5	40	69.0	281	2	O9KPY3
6	40	69.0	305	2	O45818
7	40	69.0	400	2	P74474
8	40	69.0	518	5	O02622
9	40	69.0	750	2	O9REPI
10	40	69.0	1451	5	O01737
11	39	67.2	73	14	O9DMY8
12	39	67.2	191	2	O9EW89
13	39	67.2	228	2	O59962
14	39	67.2	236	2	O9RXG5
15	39	67.2	259	2	P70874
16	39	67.2	281	11	O55126
17	39	67.2	285	4	O43801
18	39	67.2	286	4	O75323
19	39	67.2	288	13	Q9PU58

20	39	67.2	335	2	O08346
21	39	67.2	335	2	O9RMA4
22	39	67.2	358	13	O9W616
23	39	67.2	358	13	O9PW55
24	39	67.2	362	13	O9W617
25	39	67.2	366	13	O9DFC6
26	39	67.2	367	13	O9DFC5
27	39	67.2	367	13	O9PD36
28	39	67.2	469	1	O50200
29	39	67.2	545	10	O9ZPS2
30	39	67.2	559	10	O9SDN4
31	39	67.2	580	10	O04585
32	39	67.2	580	10	O9ZTX4
33	39	67.2	1081	2	O9PWS7
34	38	65.5	73	14	O9DMY4
35	38	65.5	209	2	P73834
36	38	65.5	255	10	O9FL76
37	38	65.5	295	5	O9U2E7
38	38	65.5	310	2	O45279
39	38	65.5	317	2	P97024
40	38	65.5	320	2	O9FAY6
41	38	65.5	329	2	O9RKH9
42	38	65.5	336	5	O9VVK6
43	38	65.5	498	2	O87798
44	38	65.5	501	2	O07068
45	38	65.5	569	5	O62270

ALIGNMENTS

RESULT 1
ID Q9S1E4 PRELIMINARY; PRT; 902 AA.
AC Q9S1E4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE NREI PROTEIN.
GN NREI
OS Wolinella succinogenes.
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Wolinella.
OX NCBI_Taxid=844;
RN [1]
RP SEQUENCE FROM N.A.
RA Simon J., Gross R., Einsle O., Kroneck P.M.H., Kroeger A., Klimek O.;
RT "A NapC/NirT-type cytochrome c (NirH) is the mediator between the
RT quinine pool and the cytochrome c nitrite reductase of Wolinella
RT succinogenes.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ245540; CAB53161.1; -;
DR InterPro; IPR001064; -;
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN.1.
SQ SEQUENCE 902 AA; 102016 MW; D2621BF042288380 CRC64;

Query Match 72.4%; Score 42; DB 2; Length 902;
Best Local Similarity 62.5%; Pred. No. 74;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTWGQYMA 8
DB 794 ESMGRYMA 801
RESULT 2
ID Q9UVZ4 PRELIMINARY; PRT; 116 AA.
AC Q9UVZ4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE XYLANASE (FRAGMENT).
GN AXIL2.
OS Gaumannomyces graminis.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes Incertae sedis; Magnaporthaceae; Gaumannomyces.
OK NCBI_TaxID=29850;
RN [1]
RP SEQUENCE FROM N.A.
RA Emami K.;
RT "PCR-based characterization of fungal xylanase genes."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ249160; CAB53513.1; -.
DR HSSP; P09850; 1XNB.
DR InterPro; IPR001137; -.
DR Pfam; PF00457; Glyco_hydro.11; 1.
DR PRINTS; PR00911; GLYHDBLASE1.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
FT NON_TER 1
FT 116 116
SQ SEQUENCE 116 AA; 12791 MM; DA7BA4FEA6770E9E CRC64;

Query Match 70.7%; Score 41; DB 3; Length 116;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYMAV 9
II: IIII:
DB 80 KTFNGYMAI 88

RESULT 3
ID 018533 PRELIMINARY; PRT; 458 AA.
AC 018533:
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE PREPROCATHEPSIN C PRECURSOR (EC 3.4.14.1).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
OC Trematoda; Digenea; Strigoida; Schistosomatidae; Schistosomatidae;
OC Schistosoma.
OK NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CHINESE;
RX MEDLINE=97442731; PubMed=9297696;
RA Brindley P.J., Kalina B.H., Dalton J.P., Day S.R., Wong J.Y.,
RT Smythe M.L., Mcmanus D.P.;
RL "Proteolytic degradation of host hemoglobin by schistosomes.";
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CHINESE;
RA Hota-Jamiska L., Dalton J.P., Askov J., Day S.R., Fan J.,
RL Brindley P.J.;
DR Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U7932; AAC32040.1; -.
DR HSSP; P00787; THE.
DR InterPro; IPR000169; -.
DR InterPro; IPR000668; -.
DR Pfam; PF00112; Peptidase_C1; 1.
DR PRINTS; PS00705; PAPA1N.
DR PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
DR Hydrolase; Signal; Thiol protease.
FT SIGNAL 1 26
FT CHAIN 222 458 CATEPSIN C.
SQ SEQUENCE 458 AA; 52698 MM; ADA9765666C4142C CRC64;

Query Match 70.7%; Score 41; DB 5; Length 458;

Best Local Similarity 83.3%; Pred. No. 54;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 TWGQY 7
IIIIII
DB 425 SWGQY 430

RESULT 4
ID 0919N5 PRELIMINARY; PRT; 276 AA.
AC 0919N5:
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE 276AA LONG HYPOTHETICAL LACTOSE TRANSPORT SYSTEM PERMEASE PROTEIN.
GN APER2253.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
OC Aeropyrum.
OK NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K1.
RX MEDLINE=99310339; PubMed=10382966;
RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Halkawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Anka A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
crenarchaeon, Aeropyrum pernix K1.";
RL DNA Res. 6:83-101(1999).
DR EMBL; AP000064; BAA81265.1; -.
DR InterPro; IPR000515; -.
DR Pfam; PF00528; BPD_transp; 1.
SQ SEQUENCE 276 AA; 31573 MM; A94B6CBF8032631 CRC64;

Query Match 69.0%; Score 40; DB 1; Length 276;
Best Local Similarity 55.6%; Pred. No. 46;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYMAV 9
IIIIII:
DB 215 RTWGQYMAI 223

RESULT 5
ID 09KPY3 PRELIMINARY; PRT; 281 AA.
AC 09KPY3:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE HYPOTHETICAL PROTEIN VC2229.
GN VC2229.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OK NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-EL TOR N1961 / SEROTYPE O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva L.D., Vamathevan J., Bass S., Qin H., Dracot I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RT Fraser C.M.;
RL "DNA sequence of both chromosomes of the cholera pathogen Vibrio

RT cholerae.";
 RL Nature 406:477-483(2000).
 DR EMBL: AE004294; AAF55373.1;
 DR TIGR: VC2229;
 SQ SEQUENCE 281 AA; 31824 MW; 7CAV5AD3494DFDD0 CRC64;

Query Match
 Best Local Similarity 100.0%; Score 40; DB 2; Length 281;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 WGOY 7
 |||||
 Db 99 WGOY 103

RESULT 6
 ID 045818 PRELIMINARY; PRT; 305 AA.
 AC 045818;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE HYPOTHETICAL 33.7 KDA PROTEIN (BGHC).
 GN BGHC.
 OS Chloroflexus aurantiacus.
 OC Bacteria; Green non-sulfur bacteria; Chloroflexaceae group;
 OC Chloroflexaceae; Chloroflexus.
 OX NCBI_TaxID=1108;
 RN [1]
 RP SEQUENCE OF 224-305 FROM N.A.
 RC STRAIN-J10-FL;
 RA Niedecker G., Shiozawa J., Lottspeich F., Feick R.;
 RT "The primary structure of two chlorosome proteins from Chloroflexus
 aurantiacus.";
 RL FEBS Lett. 342:61-65(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-J10-FL;
 RA Niedecker G.;
 RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC MEDLINE-94192803; PubMed-7511541;
 RA Niedecker G., Shiozawa J.A., Lottspeich F., Feick R.G.;
 RT "The primary structure of two chlorosome proteins from Chloroflexus
 aurantiacus.";
 RL FEBS Lett. 342:61-65(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC MEDLINE-20433268; PubMed-10976061;
 RA Xiong J., Fischer W.M., Inoue K., Nakahara M., Bauer C.E.;
 RT "Molecular evidence for the early evolution of photosynthesis.";
 RL Science 289:1724-1730(2000).
 DR EMBL: 234000; CAA83969.1;
 DR EMBL: AF288602; AAG15233.1;
 DR InterPro: IPR000537;
 DR Pfam: PF01040; UblA; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 305 AA; 33674 MW; F990F92P2D1C2B07 CRC64;

Query Match
 Best Local Similarity 100.0%; Score 40; DB 2; Length 305;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 WGOY 7
 |||||
 Db 246 WGOY 250

RESULT 7

P74474
 ID P74474 PRELIMINARY; PRT; 400 AA.
 AC P74474;
 DT 01-FEB-1997 (TREMblrel. 02, Created)
 DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)
 DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
 DE D-ALANYL-D-ALANINE CARBOXYPEPTIDASE.
 GN SUR1924.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE-97061201; PubMed-8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hirosewa M., Sugita M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
 RA Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 Synechocystis sp. strain PCC6803. II. Sequence determination of the
 entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 DR EMBL: D90915; BAA18575.1;
 DR MEROPS: S12.001;
 KW Carboxypeptidase.
 SQ SEQUENCE 400 AA; 44316 MW; 75510481820E462F CRC64;

Query Match
 Best Local Similarity 100.0%; Score 40; DB 2; Length 400;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 WGOY 7
 |||||
 Db 335 WGOY 339

RESULT 8
 ID 002622 PRELIMINARY; PRT; 518 AA.
 AC 002622;
 DT 01-JUL-1997 (TREMblrel. 04, Created)
 DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)
 DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
 DE ALPHA-AMYLASE PRECURSOR (EC 3.2.1.1) (1/4-ALPHA-D-GLUCAN
 DE GLUCANOHYDROLASE) (GLYCOGENASE) (FRAGMENT).
 GN AMY.
 OS Crassostrea gigas (Pacific oyster).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;
 OC Ostreoida; Ostreidae; Crassostrea.
 OX NCBI_TaxID=29159;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-DIGESTIVE GLAND;
 RA Moal J., Daniel J.Y., Le Moine S., Sellios D., Van Wormhoudt A.,
 RA Samain J.F.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOMYDOLYSIS OF 1,4-ALPHA-GLUCOSIDIC
 LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
 DR EMBL: Y08370; CAA69658.1;
 DR HSP: P00690; 1FH;
 DR InterPro: IPR000461;
 DR Pfam: PF00128; alpha-amylase; 1.
 DR PRINTS: PR00110; ALPHAAMYLASE.
 KW Signal: Hydrolase; Glycosidase.
 FT NON_TER 1
 FT SIGNAL <1 18
 FT CHAIN 19 518 POTENTIAL ALPHA-AMYLASE.
 SQ SEQUENCE 518 AA; 57435 MW; 2F3864914E77278AC CRC64;

Query Match
 Best Local Similarity 100.0%; Score 40; DB 5; Length 518;

Best Local Similarity 55.6%; Pred. No. 87;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 KTMGOYMAV 9
|||||:
DB 292 KTMGEOMGM 300

RESULT 9
O9REPI PRELIMINARY; PRT; 750 AA.

AC O9REPI 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE FERRECHROME RECEPTOR FCUA PRECURSOR.
GN FCUA.
OS Zymomonas mobilis.
OC Bacteria; Proteobacteria; alpha subdivision; Sphingomonas group;
OX Zymomonas.
RN NCB1_TaxID=542;
RP SEQUENCE FROM N.A.
RC STRAIN-ZM4;
RA Um H.W., Kang H.S.;
RT "Sequence analysis of 42B3 fosmid clone of Zymomonas mobilis."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF213822; AAF23804.1; -
KW Receptor.
SQ SEQUENCE 750 AA; 82315 MW; 272729049A69FCED CRC64;

Query Match 69.0%; Score 40; DB 2; Length 750;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KTMGOYMA 8
|||||:
DB 313 KTMGOYMA 320

RESULT 10
O01737 PRELIMINARY; PRT; 1451 AA.

AC O01737 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE F20H11.2 PROTEIN.
GN F20H11.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCB1_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Wilson R., Moesner J., Graves T.;
RT "The sequence of C. elegans cosmid F20H11."
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF002197; AAD34660.1; -
SQ SEQUENCE 1451 AA; 161680 MW; BCC3557BD68F8E01 CRC64;

Query Match 69.0%; Score 40; DB 5; Length 1451;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 WGOYMA 8
|||||:
DB 572 WGOYMA 577

RESULT 11
O9DMY8 PRELIMINARY; PRT; 73 AA.

AC O9DMY8 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE MAJOR CAPSID PROTEIN L1 (FRAGMENT).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OX NCB1_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-EA50;
RA Antonsson A., Hossain S., Simon M., Hansson B.G.;
RT "Skin HPV found on foreheads."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY009882; AAG27044.1; -
FT NON_TER
FT 1 73
SQ SEQUENCE 73 AA; 8479 MW; F1D5B6307D39062 CRC64;

Query Match 67.2%; Score 39; DB 14; Length 73;
Best Local Similarity 71.4%; Pred. No. 17;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 WGOYMAV 9
|||||:
DB 42 WGOYMAV 48

RESULT 12
O9EW89 PRELIMINARY; PRT; 191 AA.

AC O9EW89 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE BETA-XYLANASE (EC 3.2.1.8) (FRAGMENT).
GN GXYN1.
OS Streptomyces olivaceoviridis (Streptomyces corchorus11).
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCB1_TaxID=1921;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-E-86;
RA Bin Y.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-E-86;
RA Zhang H., Yao B., Wang Y.;
RT "Cloning and expression of the 23kD beta-xylanase gene from
Streptomyces olivaceoviridis E-86."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ292317; CAC19491.1; -
KW Xylan degradation; Hydrolase; Glycosidase.

FT NON TER 1 1
SQ SEQUENCE 191 AA; 20781 MW; 7E1C45AADE1B6B9C CRC64;

Query Match
Best Local Similarity 67.2%; Score 39; DB 2; Length 191;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTMGOYNAV 9
DB 131 KTFNOYMSV 139

RESULT 13
Q59962 PRELIMINARY; PRT; 228 AA.

AC Q59962;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DE ENDO-1,4-BETA-XYLANASE (EC 3.2.1.8) (1,4-BETA-D-XYLAN
GN XYLANOXYDROLASE).
OS Streptomyces sp.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1931;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=538;
RA Georjia J.C.E.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
LINKAGES IN XYLANS.
DR EMBL; X9518; CAAG7143.1; -
DR HSSP; P09850; 1XNB.
DR InterPro; IPR001137; -
DR Pfam; PF00457; GLYCO_HYDROL_11; 1.
DR PRINTS; PR00911; GLYHIDRLASE1.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KM Xylan degradation; Hydrolase; Glycosidase.
FT CHAIN 39 228 ENDO-1,4-BETA-XYLANASE.
SQ SEQUENCE 228 AA; 24493 MW; EAA15233052E744A CRC64;

Query Match
Best Local Similarity 67.2%; Score 39; DB 2; Length 228;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTMGOYNAV 9
DB 169 KTFNOYMSV 177

RESULT 14
Q9RXG5 PRELIMINARY; PRT; 236 AA.

AC Q9RXG5;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE CYTOCHROME C-TYPE BIOGENESIS PROTEIN, HEME EXPORTER PROTEIN C.
GN DR0348.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Haft D.H., Gwin M.L., Nelson W.C., Richardson D.L.,

RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Yamathaven J.J., Lam P., McDonald L., Utterback T., Zaleski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1.";
RL Science 286:1571-1577(1999).
DR EMBL; AE001895; AAF09930.1; -
DR TIGR; DR0348; -
DR InterPro; IPR002541; -
DR InterPro; IPR003557; -
DR Pfam; PF01578; CytC_asm.1.
DR PRINTS; PR01386; CCMCBIOGNIS.
SQ SEQUENCE 236 AA; 26591 MW; 18E9BD37E12CE711 CRC64;

Query Match
Best Local Similarity 83.3%; Score 39; DB 2; Length 236;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TWGOYNAV 7
DB 101 TWGOYNAV 106

RESULT 15
P70874 PRELIMINARY; PRT; 259 AA.

AC P70874;
DT 01-FEB-1997 (TREMblrel. 02, Created)
DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)
DE SPORE CORTEX-LYTIC ENZYME PREPEPTIDE PRECURSOR (GERMINATION-SPECIFIC
DE AMIDASE) (SCLF).
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/staphylococcus group; Bacillus.
OX NCBI_TaxID=1396;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 33-52; 64-80; 83-94 AND 215-234.
RC STRAIN=IFO 13597;
RX MEDLINE=96359394; PubMed=8752358;
RA Moriyama R., Kudoh S., Miyata S., Nonobe S., Hattori A., Makino S.;
RT "A germination-specific spore cortex-Lytic enzyme from Bacillus cereus
RT spores: cloning and sequencing of the gene and molecular
RT characterization of the enzyme.";
RL J. Bacteriol. 178:5330-5332(1996).
CC -1- FUNCTION: PROBABLE N-ACETYLTRANSFERASE-L-ALANINE AMIDASE. DEGRADATES
DECOATED SPORES DERIVED FROM VARIOUS ORGANISMS. PRESENT IN DORMANT
CC SPORES IN ITS ACTIVE FORM.
CC -1- SUBCELLULAR LOCATION: SPORE-BOUND.
DR EMBL; D63645; BAA09800.1; -
DR InterPro; IPR002477; -
DR Pfam; PF01471; PG_binding_1; 1.
KM Hydrolase; Cell wall; Signal; Repeat.
FT SIGNAL 1 32
FT CHAIN 33 259
FT DOMAIN 33 100 SPORE-CORTEX-LYTIC ENZYME.
FT DOMAIN 65 96 MOTIF A.
FT REPEAT 65 72 2 X 8 AA APPROXIMATE REPEATS.
FT REPEAT 88 96
FT DOMAIN 154 223 MOTIF B.
SQ SEQUENCE 259 AA; 28257 MW; 36F266D32EDA544E CRC64;

Query Match
Best Local Similarity 71.4%; Score 39; DB 2; Length 259;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 WGOYNAV 9
DB 111

Db 70 WGYWAL 76

RESULT 16
ID 055126 PRELIMINARY; PRT; 281 AA.
AC 055126;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, last sequence update)
DT 01-NOV-1998 (TREMBLrel. 12, last annotation update)
DE 4-NTTROPHEMYLPHOSPHATASE DOMAIN AND NON-NEURONAL SNAP25-LIKE PROTEIN 2
(NIPSNA2 PROTEIN).
GN GBAS OR NIPSNA2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Seroussi E., Pan H.Q., Kedra D., Roe B., Dumanaki J.P.;
RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ001261; CAA04635.1; -
DR MGD; MGI:1278343; Gbas.
SQ SEQUENCE 281 AA; 32932 MW; 260D52675BF1CA7E CRC64;

Query Match 67.2%; Score 39; DB 11; Length 281;
Best Local Similarity 83.3%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 WGOYWA 8
Db 197 WGNWYA 202

RESULT 17
ID 043801 PRELIMINARY; PRT; 285 AA.
AC 043801;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, last annotation update)
DE NIPSNA2 PROTEIN.
GN NIPSNA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Seroussi E., Pan H.Q., Kedra D., Roe B., Dumanaki J.P.;
RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ001259; CAA04633.1; -
DR InterPro; IPR001066; -
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
SQ SEQUENCE 285 AA; 33769 MW; B83CD282EA759D2D CRC64;

Query Match 67.2%; Score 39; DB 4; Length 285;
Best Local Similarity 83.3%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 WGOYWA 8
Db 201 WGNWYA 206

RESULT 18
ID 075323 PRELIMINARY; PRT; 286 AA.
AC 075323;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)

DT 01-NOV-1998 (TREMBLrel. 08, last annotation update)
DE GBAS.
GN GBAS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277458; PubMed=9615231;
RA Wang X.Y., Smith D.T., Liu W., James C.D.;
RT "GBAS, a novel gene encoding a protein with tyrosine phosphorylation
sites and a transmembrane domain, is co-amplified with Esfr.;"
RL Genomics 49:448-451(1998).
DR EMBL; AF029786; AAC29002.1; -
SQ SEQUENCE 286 AA; 33742 MW; 7ED85297E4DC9D08 CRC64;

Query Match 67.2%; Score 39; DB 4; Length 286;
Best Local Similarity 83.3%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 WGOYWA 8
Db 202 WGNWYA 207

RESULT 19
ID 09P058 PRELIMINARY; PRT; 288 AA.
AC 09P058;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)
DE NIPSNA2 PROTEIN (FRAGMENT).
GN NIPSNA2.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes;
OC Cypriniformes; Cyprinidae; Rasbora; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Kedra D., Dumanaki J.P.;
RT "Cloning of NIPSNA2 gene orthologues in Danio rerio and Drosophila
melanogaster."
RL Submitted (Sep-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ249797; CAB56702.1; -
DR InterPro; IPR001781; -
DR PRODOM; PD000094; -; 1.
FT NON_TER 1 1
SQ SEQUENCE 288 AA; 33667 MW; 66EDDBB045C6288C CRC64;

Query Match 67.2%; Score 39; DB 13; Length 288;
Best Local Similarity 83.3%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 WGOYWA 8
Db 204 WGNWYA 209

RESULT 20
ID 008346 PRELIMINARY; PRT; 335 AA.
AC 008346;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)
DE XYLANSSE PRECURSOR (EC 3.2.1.8) (ENDO-1,4-BETA-XYLANSSE) (1,4-BETA-D-XYLAN XYLANSSE HYDROLASE).
GN XYLII.

OS Streptomyces thermoviolaceus.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1952;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OPC-520;
 RX MEDLINE=97176398; PubMed=9023944;
 RA Tsujibo H., Ohtsuki T., Ito T., Yamazaki I., Miyamoto K., Sugiyama M.,
 Tamori Y.;
 RT "Cloning and sequence analysis of genes encoding xylanases and acetyl
 xylan esterase from Streptomyces thermoviolaceus OPC-520."
 RL Appl. Environ. Microbiol. 63:661-664(1997).
 CC -1- CATALYTIC ACTIVITY: ENDOMYDOLYSIS OF 1,4-BETA-D-XYLOSIDIC
 LINKAGES IN XYLANS.
 DR EMBL: D85897; BAI19778.1; -
 DR HSSP: P09850; 1XB.
 DR InterPro: IPR001137; -
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLYHDLASE1.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW Signal: xylan degradation; Hydrolase; Glycosidase.
 FT SIGNAL 1 29
 FT CHAIN 30 335
 FT SEQUENCE 335 AA; 35280 MW; BBC9A0C2BA02341 CRC64;

Query Match 67.2%; Score 39; DB 2; Length 335;
 Best Local Similarity 66.7%; Pred. No. 81;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KTMGOYAV 9
 Db 170 KTFNOYMSV 178

RESULT 21
 ID Q9RMM4 PRELIMINARY; PRT; 335 AA.
 AC Q9RMM4;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE XYLANASE B PRECURSOR.
 CN XYNB.
 OS Streptomyces thermocyanoviolaceus.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=106355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KCM 40049;
 RA Shin J.-H., Choi J.-H., Lee O.-S., Joo G.-J., Rhee I.-K.;
 RT "Streptomyces thermocyanoviolaceus xynb (xylanase B)."
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF194025; AF04601.1; -
 DR HSSP: P09850; 1XB.
 DR InterPro: IPR001137; -
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLYHDLASE1.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW Signal: xylan degradation; Hydrolase; Glycosidase.
 FT SIGNAL 1 40
 FT CHAIN 41 335
 FT SEQUENCE 335 AA; 35328 MW; D7DED7BAFCB52710 CRC64;

Query Match 67.2%; Score 39; DB 2; Length 335;
 Best Local Similarity 66.7%; Pred. No. 81;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KTMGOYAV 9
 Db 170 KTFNOYMSV 178

RESULT 22
 ID Q9W616 PRELIMINARY; PRT; 358 AA.
 AC Q9W616;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE SIGNALING MOLECULE LEFTY1.
 CN LEFT1.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Rasbora; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bisgrove B.W., Essner J.J., Yost H.J.;
 RT "Regulation of axis development by antagonism of lefty and nodal
 signaling in the midline."
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
 DR EMBL: AF132444; A0434388.1; -
 DR HSSP: P01137; 1KLA.
 DR InterPro: IPR001111; -
 DR InterPro: IPR001839; -
 DR Pfam: PF00019; TGF-beta; 1.
 DR Pfam: PF00688; TGF-beta; 1.
 DR PROSITE: PD00357; -1.
 DR PROSITE: PS00250; TGF-beta; 1.
 DR SMART: SM00204; TGF-beta; 1.
 KW Glycoprotein.
 SO SEQUENCE 358 AA; 41018 MW; F7A86F8E828092A8 CRC64;

Query Match 67.2%; Score 39; DB 13; Length 358;
 Best Local Similarity 62.5%; Pred. No. 86;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 2 TWGOYAV 9
 Db 278 TWGOYAV 285

RESULT 23
 ID Q9PW55 PRELIMINARY; PRT; 358 AA.
 AC Q9PW55;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE ANTRIN.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Rasbora; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=99065494; PubMed=9847237;
 RA Thisse C., Thisse B.;
 RT "Antriv, a novel and divergent member of the TGFbeta superfamily,
 RT negatively regulates mesoderm induction."
 RL Development 126:229-240(1999).
 CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
 DR EMBL: AF172069; A047114.1; -
 DR HSSP: P01137; 1KLA.
 DR InterPro: IPR001111; -
 DR InterPro: IPR001839; -

DR Pfam: PF00019; TGF-beta; 1.
 DR Pfam: PF00688; TGF-propeptide; 1.
 DR PROSITE: PS00250; TGF_BETA; 1.
 DR SMART: SM00204; TGFb; 1.
 KW Glycoprotein.
 SQ SEQUENCE 358 AA; 41041 MW; 74D3036F18D2458F CRC64;

Query Match 67.2%; Score 39; DB 13; Length 358;
 Best Local Similarity 62.5%; Pred. No. 86;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 TWGOYVAV 9
 |||||
 Db 278 TWTOYWI 285

RESULT 24

O9W617 PRELIMINARY; PRT; 362 AA.

AC O9W617;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE SIGNALING MOLECULE LEFTY2.
 GN LEFTY.
 OS Brachydanio rerio (zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Rasbora; Danio.
 OC NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Biströme B.W., Essner J.J., Yost H.J.;
 RT "Regulation of axis development by antagonism of Lefty and nodal
 RT signaling in the midline."
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBD databases.
 CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
 DR EMBL: AF134445; AAD34389.1; -
 DR HSSP: P08112; 2TGF.
 DR InterPro: IPR001111; -
 DR InterPro: IPR001839; -
 DR Pfam: PF00019; TGF-beta; 1.
 DR Pfam: PF00688; TGF-propeptide; 1.
 DR PROSITE: PS00250; TGF_BETA; 1.
 DR SMART: SM00204; TGFb; 1.
 KW Glycoprotein.
 SQ SEQUENCE 362 AA; 41459 MW; 0C12B8CB3CEB6007 CRC64;

Query Match 67.2%; Score 39; DB 13; Length 362;
 Best Local Similarity 62.5%; Pred. No. 87;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 TWGOYVAV 9
 |||||
 Db 281 TWTOYWI 288

RESULT 25

O9DFC6 PRELIMINARY; PRT; 366 AA.

AC O9DFC6;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE TGF-BETA FAMILY MEMBER LEFTY-A.
 GN Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=20341055; PubMed=10882517;
 RA Branford W.W., Essner J.J., Yost H.J.;
 RT "Regulation of gut and heart left-right asymmetry by context-dependent
 RT interactions between Xenopus Lefty and BMP4 signaling."
 RL Dev. Biol. 223:291-306(2000).
 DR EMBL: AF283562; AAG10034.1; -
 SQ SEQUENCE 366 AA; 41434 MW; E65CEC306F4B5ED5 CRC64;

Query Match 67.2%; Score 39; DB 13; Length 366;
 Best Local Similarity 62.5%; Pred. No. 88;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 TWGOYVAV 9
 |||||
 Db 284 TWTOYWI 291

RESULT 26

O9DFC5 PRELIMINARY; PRT; 367 AA.

AC O9DFC5;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE TGF-BETA FAMILY MEMBER LEFTY-B.
 GN Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Branford W.W., Essner J.J., Yost H.J.;
 RT "Regulation of gut and heart left-right asymmetry by context-dependent
 RT interactions between Xenopus Lefty and BMP4 signaling."
 RL Dev. Biol. 223:291-306(2000).
 DR EMBL: AF283563; AAG10035.1; -
 SQ SEQUENCE 367 AA; 41604 MW; DBA7E85752B7B3A CRC64;

Query Match 67.2%; Score 39; DB 13; Length 367;
 Best Local Similarity 62.5%; Pred. No. 88;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 TWGOYVAV 9
 |||||
 Db 284 TWTOYWI 291

RESULT 27

O9DD36 PRELIMINARY; PRT; 367 AA.

AC O9DD36;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE XANTIVIN (LEFTY-RELATED FACTOR XATV).
 GN XANTIVIN.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tanegashima K., Yokota C., Takahashi S., Asashima M.;
 RT "Expression cloning of Xantivn, a Xenopus lefty/xantivn-related gene,
 RT involved in the regulation of activin signaling during mesoderm
 induction."

RL Mech. Dev. 99:3-14(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Cheng A.M.S., Thisse B., Thisse C., Wright C.V.E.;
 RT "The lefty-related factor Xatv acts as a feedback inhibitor of nodal
 signaling in mesoderm induction and L-R axis development in Xenopus.";
 RL Development 0:0-0(2000).
 DR EMBL: AB038010; BAB12725.1; -
 DR EMBL: AF209744; AAG35771.1; -
 SQ SEQUENCE 367 AA; 41504 MW; DEAA90275BC8574A CRC64;

Query Match 67.2%; Score 39; DB 13; Length 367;
 Best Local Similarity 62.5%; Pred. No. 88;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 TWGQYAV 9
 DB 284 TWGQYAV 291

RESULT 28
 ID 050200 PRELIMINARY; PRT; 469 AA.
 AC 050200;
 DT 01-JUN-1998 (TREMblrel. 06, Created)
 DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
 DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
 DE AMYLASE (EC 3.2.1.1) (ALPHA-AMYLASE) (1,4-ALPHA-D-GLUCAN
 DE GLUCANOHYDROLASE) (GLYCOGENASE).
 GN AMY.
 OS Thermococcus sp. R3.
 OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Thermococcus.
 OX NCBI_TaxID=65421;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RT3;
 RA Jones R.A., Patel B., Beacham I.R.;
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 CC -1 CATALYTIC ACTIVITY: ENDOLYSIN OF 1,4-ALPHA-GLUCOSIDIC
 CC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
 DR EMBL: AF017454; AAB87860.1; -
 DR HSSP: P06278; IVJS.
 DR InterPro: IPR000461; -
 DR Pfam: PF00128; alpha-amylase; 1.
 KW Hydrolase; Glycosidase.
 SQ SEQUENCE 469 AA; 52756 MW; C3B0614FBA4DB3E2 CRC64;

Query Match 67.2%; Score 39; DB 1; Length 469;
 Best Local Similarity 71.4%; Pred. No. 11e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYV 7
 DB 204 KSMQYV 210

RESULT 29
 ID 092PS2 PRELIMINARY; PRT; 545 AA.
 AC 092PS2;
 DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
 DE PUTATIVE OLIGOPEPTIDE TRANSPORT PROTEIN.
 GN F14H20.9.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
 RA Barnstead M.E., Mason T.M., Bowman C.L., Rongling C.M., Benito M.,
 RA Carrera A.J., Greasy T.H., Buell C.R., Town C.D., Mierman W.C.,
 RA Fraser C.M., Venter J.C.;
 RT "Arabidopsis thaliana chromosome II BAC F14H20 genomic sequence.";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC006532; AAD20094.1; -
 DR InterPro: IPR000109; -
 DR Pfam: PF00854; PTR2; 2.
 DR PROSITE: PS01022; PTR2.1; 1.
 DR PROSITE: PS01023; PTR2.2; UNKNOWN.1.
 SQ SEQUENCE 545 AA; 60879 MW; E69740E3A53FEA5F CRC64;

Query Match 67.2%; Score 39; DB 10; Length 545;
 Best Local Similarity 57.1%; Pred. No. 1.3e+02;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 WGOYAV 9
 DB 111 WGOYAV 117

RESULT 30
 ID 09SDN4 PRELIMINARY; PRT; 559 AA.
 AC 09SDN4;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMblrel. 14, Last annotation update)
 DE AMINO ACID/PEPTIDE TRANSPORTER.
 GN PTR2.
 OS Prunus dulcis (Almond) (Prunus amygdalus).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
 OC Rosales; Rosaceae; Prunus.
 OX NCBI_TaxID=3755;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Campalans A., Pages M., Messegue R.;
 RT "Identification of differentially expressed genes during dehydration
 RT in almond (Prunus amygdalus) using the cDNA-AFLP technique.";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF213936; AAR20002.1; -
 DR InterPro: IPR000109; -
 DR Pfam: PF00854; PTR2; 1.
 DR PROSITE: PS01022; PTR2.1; 1.
 DR PROSITE: PS01023; PTR2.2; 1.
 SQ SEQUENCE 559 AA; 61604 MW; AAB9D08BD085C9A3 CRC64;

Query Match 67.2%; Score 39; DB 10; Length 559;
 Best Local Similarity 57.1%; Pred. No. 1.4e+02;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 WGOYAV 9
 DB 110 WGOYAV 116

Search completed: July 3, 2001, 10:28:10
 Job time: 330 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2001, 10:00:55 ; Search time 23.85 Seconds
(without alignments)
28.745 Million cell updates/sec

Title: US-09-214-836-1

Perfect score: 58

Sequence: 1 KTWGQYNAV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: pirl:*
2: pirl:*
3: pirl:*
4: pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	91.4	662	2 I38400	melanoma-associated
2	53	91.4	668	2 A41234	melanocyte-specific
3	49	84.5	626	2 S53871	Pmel 17 protein -
4	42	72.4	305	2 C69708	spore cortex-lytic
5	42	72.4	315	2 T07314	cytochrome c-type
6	40	69.0	264	2 H85861	hypothetical prote
7	40	69.0	276	2 A72451	probable lactose t
8	40	69.0	281	2 A82104	conserved hypothet
9	40	69.0	305	1 S52775	hypothetical prote
10	40	69.0	400	2 S76446	hypothetical prote
11	40	69.0	549	2 H64992	hypothetical prote
12	40	69.0	807	2 F64844	yods protein precu
13	40	69.0	807	2 F85648	probable outer mem
14	39	67.2	208	2 S46301	flucocanthin chloro
15	39	67.2	236	2 A75530	cytochrome c-type
16	39	67.2	256	2 B70750	hypothetical prote
17	39	67.2	335	1 A39862	protein-tyrosine-p
18	39	67.2	545	2 A84432	probable peptide/a
19	39	67.2	568	2 E96648	hypothetical prote
20	39	67.2	585	2 C84432	histidine transpor
21	39	67.2	586	2 S46236	histidine transpor
22	39	67.2	1081	2 B81303	probable membrane
23	38	65.5	209	2 S75029	hypothetical prote
24	38	65.5	277	1 ORECST	sulfate/rhiosulfat
25	38	65.5	277	1 ORECST	hypothetical prote
26	38	65.5	290	2 C86097	4-hydroxybenzoate-
27	38	65.5	290	2 JC2316	hypothetical prote
28	38	65.5	290	2 T22928	hypothetical prote
29	38	65.5	622	2 H64447	hypothetical prote

30	38	65.5	936	2 B64567	cytochrome c bioge
31	38	65.5	936	2 H71862	probable cytochrom
32	37	63.8	240	1 JS0591	endo-1,4-beta-xyla
33	37	63.8	241	2 T37005	endo-1,4-beta-xyla
34	37	63.8	293	2 T11969	cytochrome c-type
35	37	63.8	301	2 D82040	cysQ protein VC272
36	37	63.8	306	1 S25309	cytochrome c-type
37	37	63.8	312	2 S78242	cytochrome c-type
38	37	63.8	319	1 S73290	cytochrome c-type
39	37	63.8	320	2 T07572	hypothetical prote
40	37	63.8	322	2 T06955	probable cytochrom
41	37	63.8	324	2 D70545	probable cytochrom
42	37	63.8	325	2 F65088	hypothetical prote
43	37	63.8	327	1 S72913	cytochrome c-type
44	37	63.8	334	1 S74957	cytochrome c-type
45	37	63.8	353	2 T07998	cytochrome c-type

ALIGNMENTS

RESULT 1
I38400 melanoma-associated ME20 antigen (me20m) - human
N:Alternate names: melanoma antigen 25
C:Species: Homo sapiens (man)
C>Date: 01-Nov-1996 #sequence, revision 01-Nov-1996 #text_change 01-Dec-2000
C:Accession: I38400; A53668; A55753
R:Marsh, G.A.; Marken, J.S.; Neubauer, M.; Aruffo, A.; Hellstrom, I.; Hellstrom, K.; DNA Cell Biol. 13, 87-95, 1994
A>Title: Cloning and expression of the gene for the Melanoma-Associated ME20 Antigen.
A:Reference number: I38400; MUID:94235165
A:Accession: I38400
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-662 <RES>
A:Cross-references: EMBL:U01874; NID:9494939; PID:AAA18479.1; PID:9494940
R:Adema, G.J.; de Boer, A.J.; Vogel, A.M.; Loenen, W.A.M.; Figdor, C.G. J. Biol. Chem. 269, 20126-20133, 1994
A>Title: Molecular characterization of the melanocyte lineage-specific antigen gp100.
A:Reference number: A53668; MUID:94327568
A:Accession: A53668
A:Molecule type: mRNA
A:Residues: 1-592,594-662 <ADE>
A:Cross-references: GB:S73003; NID:9639589; PID:AMC60634.1; PID:9639590
R:Kwakami, Y.; Eliyahu, S.; Delgado, C.H.; Robins, P.F.; Sakaguchi, K.; Appella, E. Proc. Natl. Acad. Sci. U.S.A. 91, 6458-6462, 1994
A>Title: Identification of a human melanoma antigen recognized by tumor-infiltrating
A:Reference number: A55753; MUID:94294401
A:Accession: A55753
A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-161,'F',163-592,594-662 <KAW>
C:Keywords: glycoprotein

Query Match 91.4%; Score 53; DB 2; Length 662;
Best Local Similarity 88.9%; Pred. No. 0.88;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 KTWGQYNAV 9
DB 154 KTWGQYNAV 162
RESULT 2
A41234 melanocyte-specific protein Pmel-17 precursor - human
C:Species: Homo sapiens (man)
C>Date: 19-Jun-1992 #sequence, revision 19-Jun-1992 #text_change 30-Sep-1993
C:Accession: A41234
R:Kwon, B.S.; Chintamaneni, C.; Kozak, C.A.; Copeland, N.G.; Gilbert, D.J.; Jenkins, Proc. Natl. Acad. Sci. U.S.A. 88, 9228-9232, 1991

A:Title: A melanocyte-specific gene, Pmel 17, maps near the silver coat color locus on H
A:Reference number: AA1234; MUID:92021023
A:Accession: AA1234
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-668 <KMO>
A:Cross-references: GB:M77348

Query Match 91.4%; Score 53; DB 2; Length 668;
Best Local Similarity 88.9%; Pred. No. 0.89;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTWGQYMAV 9
|||||
DB 154 KTWGQYMAV 162

RESULT 3

Pmel 17 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 05-Nov-1999
C:Accession: S53871
R:Kwon, B.S.; Halaban, R.; Ponnazhagan, S.; Kim, K.; Chintamani, C.; Bennett, D.; Pick
Nucleic Acids Res. 23, 154-158, 1995
A:Title: Mouse silver mutation is caused by a single base insertion in the putative cyto
A:Reference number: S53871; MUID:95175358
A:Accession: S53871
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-626 <KMO>
A:Cross-references: GB:U14133; MID:9887940; PIDN:AAA69538.1; PID:9887941

Query Match 84.5%; Score 49; DB 2; Length 626;
Best Local Similarity 77.8%; Pred. No. 3.4;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTWGQYMAV 9
|||||
DB 154 KTWGQYMAV 162

RESULT 4

Spore cortex-lytic enzyme prepeptide [imported] - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000
C:Accession: C69708; T44770
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
leach, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y. M.; Ogawa, K.; Ogilwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon
A:Authors: Scheich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot
teuchl, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasunori, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033
A:Accession: C69708
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-305 <KUN>
A:Cross-references: GB:Z99115; GB:Z99116; GB:AL009126; MID:g2634723; PIDN:CAB14225.1; PI
R:Moriyama, R.; Hattori, A.; Miyata, S.; Kudoh, S.; Makino, S.

J. Bacteriol. 178, 6059-6063, 1996

A:Title: A gene (slrB) encoding a spore cortex-lytic enzyme from Bacillus subtilis an
A:Reference number: Z22836; MUID:96427343
A:Accession: T44770
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-305 <MOR>
A:Cross-references: EMBL:D79978; MID:g1688021; PIDN:BAAL1473.1; PID:g1688023
A:Experimental source: strain 168
A:Genetics:
A:Gene: slrB

Query Match 72.4%; Score 42; DB 2; Length 305;
Best Local Similarity 85.7%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WQGYMAV 9
|||||
DB 67 WQGYMAV 73

RESULT 5

cytochrome c-type synthesis protein homolog - Chlorella vulgaris chloroplast
C:Species: Chlorella vulgaris
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C:Accession: T07314
R:Wakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Tsudzuki, J.; Na
Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997
A:Title: Complete nucleotide sequence of the chloroplast genome from the green alga C
A:Reference number: T15985; MUID:97303241
A:Accession: T07314
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-315 <MAK>
A:Cross-references: EMBL:AB001684; MID:g2224352; PIDN:BAAS7962.1; PID:g2224478
A:Genetics:
A:Gene: ycf5
A:Genome: chloroplast
C:Superfamily: cytochrome c-type synthesis protein
C:Keywords: chloroplast

Query Match 72.4%; Score 42; DB 2; Length 315;
Best Local Similarity 62.5%; Pred. No. 20;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTWGQYMA 8
|||||
DB 243 KTWGQYMA 250

RESULT 6

hypothetical protein Z3480 [imported] - Escherichia coli (strain O157:H7)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C:Accession: H85861
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grobbeck, E.J.; Davis, N.W.; Lam, A.; Diallanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: AB5480; MUID:21074935; PMID:11206551
A:Accession: H85861
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-264 <STO>
A:Cross-references: GB:AE005174; MID:g12516559; PIDN:AAG57356.1; GSPDB:GN00145; UWGP:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z3480

Query Match 69.0%; Score 40; DB 2; Length 264;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WGOYX 7
 |||||
 Db 125 WGOYX 129

RESULT 7

A72451
 Probable lactose transport system permease protein APE2253 - Aeropyrum pernix (strain K1)
 C:Species: Aeropyrum pernix
 C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
 C:Accession: A72451
 R:Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K DNA Res. 6, 83-101, 1999
 A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum
 A:Reference number: A72450; MUID:99310339
 A:Accession: A72451
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-276 <KAN>
 A:Cross-references: DDBJ:AF000064; NID:g5105945; PIDN:BA81265.1; PID:g5105954
 A:Experimental source: strain K1
 C:Genetics:
 A:Gene: APE2253
 C:Superfamily: Inner membrane protein 199a

Query Match 69.0%; Score 40; DB 2; Length 276;
 Best Local Similarity 55.6%; Pred. No. 36;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTWGQYX 9
 :|||:|
 Db 215 RTWGQYX 223

RESULT 8

A82104
 conserved hypothetical protein VC2229 [Imported] - Vibrio cholerae (strain N16961 serogr C:Species: Vibrio cholerae
 C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 C:Accession: A82104
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F L, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A:Reference number: A82035; MUID:20406833
 A:Accession: A82104
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-281 <HEI>
 A:Cross-references: GB:AE004294; GB:AE003852; NID:g9656774; PIDN:AAF95373.1; GSPDB:GN001 C:Genetics:
 A:Gene: VC2229
 A:Map position: 1
 C:Superfamily: hypothetical protein H11037

Query Match 69.0%; Score 40; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WGOYX 7
 |||||
 Db 99 WGOYX 103

RESULT 9
 S52775
 hypothetical protein 2 - Chloroflexus aurantiacus

C:Species: Chloroflexus aurantiacus
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
 C:Accession: S52775
 R:Niedermeyer, G.; Shiozawa, J.A.; Lottspeich, F.; Felck, R.G.
 FEBS Lett. 342, 61-65, 1994
 A:Title: The primary structure of two chlorosome proteins from Chloroflexus aurantiacus
 A:Reference number: S43678; MUID:94192803
 A:Accession: S52775
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-305 <NEI>

A:Cross-references: EMBL:Z34000; NID:g496485; PIDN:CAA83969.1; PID:g496488
 A:Note: only a part of the coding sequence is given in this paper
 A:Note: the nucleotide sequence was submitted to the EMBL data library, May 1994
 C:Superfamily: Methanococcus jannaschii conserved hypothetical protein M0279

Query Match 69.0%; Score 40; DB 1; Length 305;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WGOYX 7
 |||||
 Db 246 WGOYX 250

RESULT 10

S76446
 hypothetical protein - Synechocystis sp. (strain PCC 6803)
 C:Species: Synechocystis sp.
 A:Variety: PCC 6803
 C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
 C:Accession: S76446
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O, K.; Okumura, S.; Shingo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas DNA Res. 3, 109-136, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis.
 A:Reference number: S74322; MUID:97061201
 A:Accession: S76446
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-400 <KAN>
 A:Cross-references: EMBL:D90915; GB:AB001339; NID:g1653604; PIDN:BA18575.1; PID:d101 A:Note: the nucleotide sequence was submitted to the EMBL data library, June 1996

Query Match 69.0%; Score 40; DB 2; Length 400;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WGOYX 7
 |||||
 Db 335 WGOYX 339

RESULT 11

H64992
 hypothetical protein b2226 - Escherichia coli (strain K-12)
 C:Species: Escherichia coli
 C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 04-Mar-2000
 C:Accession: H64992
 R:Battner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426617
 A:Accession: H64992
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-549 <BLAT>
A:Cross-References: GB:AE000312; GB:U00096; NID:g178855; PIDN:AC75286.1; PID:g1788557;
A:Experimental source: strain K-12, substrain MG1655
C:Superfamily: Escherichia coli hypothetical protein b2226

Query Match 69.0%; Score 40; DB 2; Length 549;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 WGOYW 7
DB 125 WGOYW 129

RESULT 12
F64844
Ycds protein precursor - Escherichia coli

C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 04-Mar-2000
C:Accession: F64844
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CC
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: F64844
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-807 <BLAT>
A:Cross-References: GB:AE000204; GB:U00096; NID:g1787256; PIDN:AC74109.1; PID:g1787261;
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: ycds
C:Superfamily: Escherichia coli ycds protein
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-807/Product: ycds protein #status predicted <MAT>

Query Match 69.0%; Score 40; DB 2; Length 807;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 WGOYW 7
DB 314 WGOYW 318

RESULT 13
F85647
Probable outer membrane protein ycds [imported] - Escherichia coli (strain O157:H7)

C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C:Accession: F85647
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grothbeck, E.J.; Davis, N.W.; Llm, A.; Dinalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: AB5480; MUID:21074935; PMID:11206551
A:Accession: F85647
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-807 <STO>
A:Cross-References: GB:AE005174; NID:g12514389; PIDN:AC655642.1; GSPDB:GN00145; UWGP:Z15
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: ycds
C:Superfamily: Escherichia coli ycds protein

Query Match 69.0%; Score 40; DB 2; Length 807;
Best Local Similarity 100.0%; Pred. No. 97;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 3 WGOYW 7
DB 314 WGOYW 318

RESULT 14
S46301
fucoxanthin chlorophyll a/c-binding light-harvesting protein - Isochrysis galbana

N:Alternate names: FCP protein
C:Species: Isochrysis galbana
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Nov-1999
C:Accession: S46301
R:Larocque, J.; Henry, D.; Wyman, K.; Suenik, A.; Falkowski, P.
Plant Mol. Biol. 25, 355-368, 1994
A:Title: Cloning and nucleotide sequence of a cDNA encoding a major fucoxanthin-, chl
e family.
A:Reference number: S46301; MUID:94325461
A:Accession: S46301
A:Molecule type: mRNA
A:Residues: 1-208 <BLAT>
A:Cross-References: EMBL:X77333; NID:g535080; PIDN:CA54547.1; PID:g535081
A:Experimental source: cultivar DUN
C:Keywords: Light-harvesting complex

Query Match 67.2%; Score 39; DB 2; Length 208;
Best Local Similarity 83.3%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TWGOYW 7
DB 198 TWGOYW 203

RESULT 15
A75330
cytochrome c-type biogenesis protein, heme exporter protein C - Deinococcus radiodurans

C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: A75330
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
M.; Shen, M.; Vamathevan, J.U.; Lam, P.; McDonald, L.; Uitterlind, T.; Zalewski, C.;
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896
A:Accession: A75330
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-236 <WHI>
A:Cross-References: GB:AE001895; GB:AE00513; NID:g6458024; PIDN:AAF09930.1; PID:g645
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0348
A:Map position: 1
C:Superfamily: helC protein

Query Match 67.2%; Score 39; DB 2; Length 236;
Best Local Similarity 83.3%; Pred. No. 45;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TWGOYW 7
DB 101 TWGOYW 106

RESULT 16
B70750
Hypothetical protein RV0090 - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis

C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 28-Jul-2000
 C/Accession: B70750
 R/Cole, S.T.; Brosch, R.; Parhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; M0ID:98295987
 A/Accession: B70750
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-256 <COL>
 A/Cross-references: GB:274410; GB:AL123456; NID:g3261600; PIDN:CAA98926.1; PID:6249404;
 C/Experimental source: strain H37Rv
 C/Genetics:
 A:Gene: RV0090
 C:Superfamily: Mycobacterium tuberculosis hypothetical protein RV0090

Query Match 67.2%; Score 39; DB 2; Length 256;
 Best Local Similarity 66.7%; Pred. No. 48;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYAV 9
 |||:|:
 Db 177 KRMGEYFV 185

RESULT 17
 A39862
 protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 1 - yeast (Saccharomyces cerevisiae)
 N/Alternate names: protein D0815; protein YDL230w
 C/Species: Saccharomyces cerevisiae
 C/Date: 30-Dec-1991 #sequence_revision 08-Mar-1996 #text_change 21-Jul-2000
 C/Accession: A39862; S67793
 R/Guan, K.; Deschenes, R.J.; Qiu, H.; Dixon, J.E.
 J. Biol. Chem. 266, 12964-12970, 1991
 A>Title: Cloning and expression of a Yeast protein tyrosine phosphatase.
 A:Reference number: A39862; M0ID:91302312
 A/Accession: A39862
 A:Molecule type: DNA
 A:Residues: 1-335 <CUA>
 A/Cross-references: GB:M64062; NID:g172295; PIDN:AAA34923.1; PID:g172296
 R/Rasmussen, S.W.
 submitted to the Protein Sequence Database, July 1996
 A:Reference number: S67778
 A/Accession: S67793
 A:Molecule type: DNA
 A:Residues: 1-335 <RAS>
 A/Cross-references: EMBL:274278; NID:g1431387; PIDN:CAA98809.1; PID:g1431388; GSPDB:GN000
 C/Experimental source: strain S288C
 C/Genetics:
 A:Gene: SGD:PTP1; MIPS:YDL230w
 A/Cross-references: SGD:S0002389; MIPS:YDL230w
 A:Map position: 4L
 C:Superfamily: Saccharomyces protein-tyrosine-phosphatase, nonreceptor type 1; protein-tyrosine-phosphatase, phosphoric monoester hydrolase; tyrosine-specific phosphatase
 C/Keywords: phosphoprotein; protein-tyrosine-phosphatase homology <RTP>
 F:52-303/Domain: protein-tyrosine-phosphatase homology <RTP>
 F:252/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:258/Binding site: substrate phosphate (Arg) #status predicted

Query Match 67.2%; Score 39; DB 1; Length 335;
 Best Local Similarity 71.4%; Pred. No. 61;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYAV 7
 |||:|:
 Db 108 KTWGQYAV 114

RESULT 18

A84432
 probable peptide/amino acid transporter [imported] - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C/Accession: A84432
 R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, B.; Koo, H.; Niemman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
 Nature 402, 761-768, 1999
 A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; M0ID:20083487
 A/Accession: A84432
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-545 <STO>
 A/Cross-references: GB:AE002093; NID:g4406784; PIDN:AAD20094.1; GSPDB:GN00139
 C/Genetics:
 A:Gene: At2g02020
 A:Map position: 2

Query Match 67.2%; Score 39; DB 2; Length 545;
 Best Local Similarity 57.1%; Pred. No. 96;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 WGOYMAV 9
 |||:|:
 Db 111 WGRYWTI 117

RESULT 19
 E96648
 hypothetical protein F19K23.13 [imported] - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C/Accession: E96648
 R/Rheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
 ansen, N.F.; Hughes, B.; Hultzer, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.; Marzia,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; M0ID:21016719
 A/Accession: E96648
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-568 <STO>
 A/Cross-references: GB:AE005173; NID:g2160144; PIDN:AAB60766.1; GSPDB:GN00141
 C/Genetics:
 A:Gene: F19K23.13
 A:Map position: 1

Query Match 67.2%; Score 39; DB 2; Length 568;
 Best Local Similarity 57.1%; Pred. No. 99;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 WGOYMAV 9
 |||:|:
 Db 106 WGRYWTI 112

RESULT 20
 C84432
 histidine transport protein (PTR2-B) [imported] - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C/Accession: C84432
 R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.

M.: Koo, H.; Mofiat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
neuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A:Reference number: A84420; MUID:20083487
A:Accession: C84432
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-585 <STO>
A:Cross-references: GB:AE002093; NID:g4406786; PIDN:AAD20096.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g02040
A:Map position: 2

Query Match 67.2%; Score 39; DB 2; Length 585;
Best Local Similarity 57.1%; Pred. No. 1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 MGQYMAV 9
|||:
Db 110 MGRYWTI 116

RESULT 21
S46236
histidine transport protein - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 21-Jul-2000
R:Frommer, W.B.; Hummel, S.; Rentsch, D.
FEBS Lett. 347, 185-189, 1994
A>Title: Cloning of an *Arabidopsis* histidine transporting protein related to nitrate and
A:Reference number: S46236; MUID:94307379
A:Accession: S46236
A:Molecule type: mRNA
A:Residues: 1-586 <PRO>
A:Cross-references: EMBL:X77503; NID:9510237; PIDN:CAA54634.1; PID:9510238
C:Genetics:
A:Gene: NTR1
C:Keywords: amino acid transport; histidine transport; transmembrane protein

Query Match 67.2%; Score 39; DB 2; Length 586;
Best Local Similarity 57.1%; Pred. No. 1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 MGQYMAV 9
|||:
Db 110 MGRYWTI 116

RESULT 22
B81303
Probable membrane protein Cj1013c [imported] - *Campylobacter jejuni* (strain NCTC 11168)
C:Species: *Campylobacter jejuni*
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000
R:Partholl, J.; Wren, B.W.; Mungall, K.; Kettle, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; O'Neill, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barre
Nature 403, 665-666, 2000
A>Title: The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hyp
A:Reference number: A81250; MUID:20150912
A:Accession: B81303
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1081 <PAR>
A:Cross-references: GB:AL139077; GB:AL111168; NID:95968444; PIDN:CAB73269.1; PID:9696844
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: Cj1013c

Query Match 67.2%; Score 39; DB 2; Length 1081;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTWGQYMA 8
|||:
Db 977 ESMGRYMS 984

RESULT 23
S75029
hypothetical protein slr2003 - *Synechocystis* sp. (strain PCC 6803)
C:Species: *Synechocystis* sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,
O.K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
DNA Res. 3, 109-136, 1996
A>Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocys*
s.
A:Reference number: S74322; MUID:97061201
A:Accession: S75029
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-209 <KAN>
A:Cross-references: EMBL:D90910; GB:AB001339; NID:g1652956; PIDN:BAA17891.1; PID:g165
C:Superfamily: *Synechocystis* hypothetical protein slr2003

Query Match 65.5%; Score 38; DB 2; Length 209;
Best Local Similarity 71.4%; Pred. No. 56;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTWGQYMA 7
|||:
Db 75 KTWQRTW 81

RESULT 24
QRECSF
sulfate/thiosulfate transport protein cyst - *Escherichia coli*
N:Alternate names: sulfate transport system permease protein cyst
C:Species: *Escherichia coli*
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999
C:Accession: A35402; G65016; B35403
R:Sirko, A.; Hryniewicz, M.; Hulanicka, D.; Boeck, A.
J. Bacteriol. 172, 3351-3357, 1990
A>Title: Sulfate and thiosulfate transport in *Escherichia coli* K-12: nucleotide sequ
A:Reference number: A35402; MUID:90264334
A:Accession: A35402
A:Molecule type: DNA
A:Residues: 1-277 <STR>
A:Cross-references: GB:M32101; GB:M38050; NID:g145657; PIDN:AAA2637.1; PID:g145659
A:Experimental source: strain K12
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A>Title: The complete genome sequence of *Escherichia coli* K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: G65016
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-277 <BLAT>
A:Cross-references: GB:AE000330; GB:U00096; NID:g1788763; PIDN:AAC75477.1; PID:g17887
A:Experimental source: strain K-12, substrain MG1655
R:Hryniewicz, M.; Sirko, A.; Paluch, A.; Boeck, A.; Hulanicka, D.
J. Bacteriol. 172, 3358-3366, 1990
A>Title: Sulfate and thiosulfate transport in *Escherichia coli* K-12: identification o
A:Reference number: A35403; MUID:90264335
A:Accession: B35403
A>Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA
 A:Residues: 1-126,'F',128-133 <HRY>
 C:Comment: This is one of the membrane-associated components of the binding protein-dep
 C:Genetics:
 A:Gene: cysU; cyst
 A:Map position: 52 min
 C:Superfamily: maltose transport protein malG
 C:Keywords: binding protein-dependent transport system; inner membrane; membrane protein

Query Match 65.5%; Score 38; DB 1; Length 277;
 Best Local Similarity 62.5%; Pred. No. 73;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 2 TWGQYMAV 9
 : | | | |
 Db 43 SMAQYMEV 50

RESULT 25
 B85885
 hypothetical protein cysU [imported] - Escherichia coli (strain O157:H7)
 C:Species: Escherichia coli
 C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
 C:Accession: B85885
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoudis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: B85885
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-277 <STO>
 A:Cross-references: GB:AE005174; NID:912516799; PIDN:AAG57542.1; GSPDB:GN00145; UMG:P.236
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: cysU
 C:Superfamily: maltose transport protein malG

Query Match 65.5%; Score 38; DB 2; Length 277;
 Best Local Similarity 62.5%; Pred. No. 73;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 2 TWGQYMAV 9
 : | | | |
 Db 43 SMAQYMEV 50

RESULT 26
 C86097
 4-hydroxybenzoate-octaprenyltransferase [imported] - Escherichia coli (strain O157:H7)
 C:Species: Escherichia coli
 C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
 C:Accession: C86097
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoudis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: C86097
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-290 <STO>
 A:Cross-references: GB:AE005174; NID:912518989; PIDN:AAG59239.1; GSPDB:GN00145; UMG:P.256
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: ubiA
 C:Superfamily: 4-hydroxybenzoate octaprenyltransferase

Query Match 65.5%; Score 38; DB 2; Length 290;

Best Local Similarity 57.1%; Pred. No. 76;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Oy 3 WGYWMSI 243
 : | | | |
 Db 237 WGYWMSI 243

RESULT 27
 JC2316
 4-hydroxybenzoate octaprenyltransferase (EC 2.5.1.-) - Escherichia coli
 C:Species: Escherichia coli
 C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Apr-2000
 C:Accession: JC2316; S24361; B42956; S25661; S31432; PC1295; I70801; G65211
 R:Suzuki, K.; Ueda, M.; Yusa, M.; Nakagawa, T.; Kawamukai, M.; Matsuda, H.
 Biosci. Biotechnol. Biochem. 58, 1814-1819, 1994
 A:Title: Evidence that Escherichia coli ubiA product is a functional homolog of yeast
 A:Reference number: JC2316; MUID:95072311
 A:Accession: JC2316
 A:Molecule type: DNA
 A:Residues: 1-290 <SUZ>
 R:Stiebert, M.; Bechtold, A.; Melzer, M.; May, U.; Berger, U.; Schroeder, G.; Schroed
 FEBS Lett. 307, 347-350, 1992
 A:Title: Ubiquinone biosynthesis. Cloning of the genes coding for chorismate pyruvate
 A:Reference number: S24360; MUID:92354744
 A:Accession: S24361
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-290 <STO>
 A:Cross-references: EMBL:X66619; NID:943230; PIDN:CAA47182.1; PID:943232
 R:Nichols, B.P.; Green, J.M.
 J. Bacteriol. 174, 5309-5316, 1992
 A:Title: Cloning and sequencing of Escherichia coli ubiC and purification of chorisma
 A:Reference number: A42956; MUID:9235505
 A:Accession: B42956
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-290 <NIS>
 A:Cross-references: GB:M93413; NID:g148106; PIDN:AAA24717.1; PID:g148108
 A:Note: Sequence extracted from NCBI backbone (NCBIN:110475, NCBI:P.110480)
 R:Nishimura, K.; Nakahigashi, K.; Inokuchi, H.
 J. Bacteriol. 174, 5762, 1992
 A:Title: Location of the ubiA gene on the physical map of Escherichia coli.
 A:Reference number: S25660; MUID:92380960
 A:Accession: S25661
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-290 <NIS>
 A:Cross-references: EMBL:X57434; NID:943233; PIDN:CAA40682.1; PID:943235
 A:Experimental source: strain K12 W3110
 A:Note: The nucleotide sequence was submitted to the EMBL Data Library, January 1991
 R:Wolter, F.
 submitted to the EMBL Data Library, November 1992
 A:Reference number: S31432
 A:Accession: S31432
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-290 <WOL>
 A:Cross-references: EMBL:X69522; NID:941180; PIDN:CAA49270.1; PID:941181
 R:Lilley, P.E.; Stamford, N.P.D.; Vasudevan, S.G.; Dixon, N.E.
 Gene 129, 9-16, 1993
 A:Title: The 92-min region of the Escherichia coli chromosome: location and cloning o
 A:Reference number: PC1295; MUID:93328130
 A:Accession: PC1295
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 48-290 <LIL>
 R:Wu, G.; Williams, H.D.; Gibson, F.; Poole, R.K.
 J. Gen. Microbiol. 139, 1795-1805, 1993
 A:Title: Mutants of Escherichia coli affected in respiration: the cloning and nucleot
 A:Reference number: I55717; MUID:94014977
 A:Accession: I70801
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-81 <RES>
A:Cross-references: GB:M96268; NID:9347886; PIDN:AAA17028.1; PID:9347889
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.F.; Burland, V.; Riley, M.; Co-
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of *Escherichia coli* K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: G65211
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-290 <BLAT>
A:Cross-references: GB:AE000477; GB:U00096; NID:92367338; PIDN:AACT7010.1; PID:91790473;
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: ubiA; cyr
A:Map position: 92 min
C:Function:
A:Description: catalyzes a key step in ubiquinone biosynthesis (condensation of octapren-
C:Superfamily: 4-hydroxybenzoate octaprenyltransferase
C:Keywords: transferase

Query Match 65.5%; Score 38; DB 2; Length 290;
Best Local Similarity 57.1%; Pred. No. 76;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 3 TWGQYMAV 9
DB 237 WGYWMSI 243

RESULT 28
T22928
hypothetical protein F58G1.7 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T22928
R:Smyle, R.
submitted to the EMBL Data Library, November 1996
A:Reference number: 219639
A:Accession: T22928
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-569 <WIL>
A:Cross-references: EMBL:Z81556; PIDN:CAB04519.1; GSPDB:GN00020; CESP:F58G1.7
A:Experimental source: clone F58G1
C:Genetics:
A:Gene: CESP:F58G1.7
A:Map position: 2
A:Introns: 49/3; 126/1; 194/3; 250/3; 401/2; 495/3

Query Match 65.5%; Score 38; DB 2; Length 569;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 TWGQYMA 8
DB 343 TWEEYMA 349

RESULT 29
H64447
hypothetical protein MJ1185 - *Methanococcus jannaschii*
C:Species: *Methanococcus jannaschii*
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: H64447
R:Butt, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
Ison, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.

A:Title: Complete genome sequence of the methanogenic archaeon, *Methanococcus jannasc*
A:Reference number: A64300; MUID:96337999
A:Accession: H64447
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-622 <BLU>
A:Cross-references: GB:U67559; GB:L77117; NID:91591798; PIDN:AAB99186.1; PID:91591812
C:Genetics:
A:Map position: REV1125034-1123166

Query Match 65.5%; Score 38; DB 2; Length 622;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 2 TWGQYMA 7
DB 24 TWGLYMA 29

RESULT 30
B64567
cytochrome c biogenesis protein - *Helicobacter pylori* (strain 26695)
C:Species: *Helicobacter pylori*
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
C:Accession: B64567
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khaliak, H.G.; Glodek, A.; McKe-
son, T.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wattey,
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
A:Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.
A:Reference number: A64520; MUID:97394467
A:Accession: B64567
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-936 <TOM>
A:Cross-references: GB:AE000554; GB:AE000511; NID:92313475; PIDN:AAD07446.1; PID:9231

Query Match 65.5%; Score 38; DB 2; Length 936;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 KTWGQYMA 7
DB 830 ESWGRYMA 836

Search completed: July 3, 2001, 10:23:12
Job time: 1337 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2001, 10:23:15 ; Search time 14.6 Seconds
(without alignments)
21.116 Million cell updates/sec

Title: US-09-214-836-1
Perfect score: 58
Sequence: 1 KTMGQYMAV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues
Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	53	91.4	PM17_HUMAN	P40967 homo sapien
2	49	84.5	PM17_MOUSE	O60696 mus musculu
3	44	75.9	PI15_CHICK	O98917 gallus galli
4	42	72.4	SLEB_BACSU	P50739 bacillus su
5	42	72.4	CCSA_CHLVV	P56315 chlorella v
6	41	70.7	CCSA_ARATH	P56770 arabidopsis
7	40	69.0	YFAQ_ECOLI	P76463 escherichia
8	40	69.0	YCD5_ECOLI	P75907 escherichia
9	39	67.2	Y090_MYCTU	P25044 saccharomyc
10	39	67.2	Y090_MYCTU	P25044 saccharomyc
11	39	67.2	Y090_MYCTU	P25044 saccharomyc
12	39	67.2	Y090_MYCTU	P25044 saccharomyc
13	38	65.5	PI2B_ARATH	P46032 arabidopsis
14	38	65.5	PI2B_ARATH	P46032 arabidopsis
15	37	63.8	UBIA_ECOLI	P16701 escherichia
16	37	63.8	XYNC_PTRLI	P26601 escherichia
17	37	63.8	CCSA_CYACA	P26220 streptomyce
18	37	63.8	CCSA_CYACA	P26220 streptomyce
19	37	63.8	CCSA_CYACA	P26220 streptomyce
20	37	63.8	CCSA_CYACA	P26220 streptomyce
21	37	63.8	CCSA_CYACA	P26220 streptomyce
22	37	63.8	CCSA_CYACA	P26220 streptomyce
23	37	63.8	CCSA_CYACA	P26220 streptomyce
24	37	63.8	CCSA_CYACA	P26220 streptomyce
25	37	63.8	CCSA_CYACA	P26220 streptomyce
26	37	63.8	CCSA_CYACA	P26220 streptomyce
27	36	62.1	PA21_BUNMU	P00619 bungarus mu
28	36	62.1	PA21_BUNMU	P00619 bungarus mu
29	36	62.1	PA21_BUNMU	P00619 bungarus mu
30	36	62.1	PA21_BUNMU	P00619 bungarus mu
31	36	62.1	PA21_BUNMU	P00619 bungarus mu
32	36	62.1	PA21_BUNMU	P00619 bungarus mu
33	36	62.1	PA21_BUNMU	P00619 bungarus mu

34	36	62.1	233	1	XYN2_MAGGR	P55335 magnaporthe
35	36	62.1	273	1	OPSR_CANFA	O18914 canis fam11
36	36	62.1	301	1	CCSA_GUTH	P22534 guillardi
37	36	62.1	313	1	CCSA_TOBAC	P12216 nicotiana t
38	36	62.1	320	1	CCSA_MARPO	P12214 marichanta
39	36	62.1	321	1	CCSA_MARZE	P46559 zea mays (m
40	36	62.1	321	1	CCSA_ORYZA	P12215 oryza sativ
41	36	62.1	463	1	SYG_MYCTU	O65932 mycobacteri
42	36	62.1	503	1	ALG2_YEAST	P43636 saccharomyc
43	36	62.1	602	1	GAP1_YEAST	P19145 saccharomyc
44	36	62.1	736	1	VM1_REOVD	P12418 reovirus (t
45	36	62.1	736	1	VM1_REOVL	O00335 reovirus (t

ALIGNMENTS

RESULT	ID	PM17_HUMAN	STANDARD	PRT	661 AA.
AC	P40967	Q16565; Q14817; Q12763; Q14448;			
DT	01-FEB-1995	(Rel. 31, Created)			
DT	01-NOV-1997	(Rel. 35, Last sequence update)			
DT	01-OCT-2000	(Rel. 40, Last annotation update)			
DE	MELANOCYTE PROTEIN PMEL 17 PRECURSOR (MELANOCYTE LINEAGE-SPECIFIC				
DE	ANTIGEN GP100) (MELANOMA-ASSOCIATED ME20 ANTIGEN) (ME20/M/ME20S)				
DE	(ME20-M/ME20-S) (95 KDA MELANOCYTE-SPECIFIC SECRETED GLYCOPROTEIN).				
GN	SLIV OR PMEL17 OR DI2553E.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID:9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=92021023; PubMed=1924386;				
RA	Kwon B.S., Chintamaneni C., Kozak C.A., Copeland N.G.,				
RA	Gilbert D.J., Jenkins N.A., Barton D., Francke U., Kobayashi Y.,				
RA	Kim K.-K.;				
RT	"A melanocyte-specific gene, Pmel 17, maps near the silver coat color				
RT	locus on mouse chromosome 10 and is in a syntenic region on human				
RT	chromosome 12."				
RL	Proc. Natl. Acad. Sci. U.S.A. 88:9228-9232(1991).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=94327568; PubMed=7519602;				
RA	Adema G.J., de Boer A.J., Vogel A.M., Loenen W.A., Fyodor C.G.;				
RA	"Molecular characterization of the melanocyte lineage-specific				
RT	antigen gp100."				
RL	J. Biol. Chem. 269:20126-20133(1994).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=96154052; PubMed=8592076;				
RA	Baillin T., Lee S.T., Spritz R.A.;				
RA	"Genomic organization and sequence of DI2553E (Pmel 17), the human				
RT	homologue of the mouse silver (sl) locus."				
RL	J. Invest. Dermatol. 106:24-27(1996).				
RN	[4]				
RP	SEQUENCE FROM N.A. AND SEQUENCE OF 25-53.				
RX	MEDLINE=94235165; PubMed=8179825;				
RA	Marresh G.A., Marken J.S., Neubauer M., Aruffo A., Hellstrom I.,				
RA	Hellstrom K.E., Marguardt H.;				
RT	"Cloning and expression of the gene for the melanoma-associated ME20				
RT	antigen."				
RL	DNA Cell Biol. 13:87-95(1994).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RX	Kwon B.S., Kim K., Heng H.H., Shi X.M., Tsui L., Lee Z.H.,				
RA	Youn B., Pickard R.T.;				
RA	Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.				
RN	[6]				
RP	SEQUENCE FROM N.A.				
RA	Vogel A.;				
RA	Submitted (NOV-1990) to the EMBL/GenBank/DBJ databases.				

CC -1- FUNCTION: COULD BE A MELANOGENIC ENZYME. COULD REPRESENT AN
CC ONCOFETAL SELF-ANTIGEN THAT IS NORMALLY EXPRESSED AT LOW LEVELS IN
CC QUIESCENT ADULT MELANOCYTES BUT OVEREXPRESSED BY PROLIFERATING
CC NEONATAL MELANOCYTES AND DURING TUMOR GROWTH. RELEASE OF THE
CC SOLUBLE FORM, ME20-S, COULD PROTECT TUMOR CELLS FROM ANTIBODY
CC MEDIATED IMMUNITY.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL). THERE
CC IS ALSO A SECRETED SOLUBLE FORM, ME20-S, PROBABLY PRODUCT OF
CC PROTEOLYTIC CLEAVAGE.
CC -1- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN MELANOMAS. SOME
CC EXPRESSION WAS FOUND IN DISPLASTIC NEVI. NOT FOUND IN NORMAL
CC TISSUES NOR IN CARCINOMAS.
CC -1- SIMILARITY: BELONGS TO THE PMEL-17/NMB FAMILY.
CC -1- SIMILARITY: CONTAINS 1 PKD DOMAIN.
CC -----
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CC -----
DR EMBL: M77348; AAC60121.1; -
DR EMBL: S73003; AAC60634.1; -
DR EMBL: U31799; AAB00386.1; -
DR EMBL: U31808; AAB00386.1; JOINED.
DR EMBL: U31807; AAB00386.1; JOINED.
DR EMBL: U31797; AAB00386.1; JOINED.
DR EMBL: U31798; AAB00386.1; JOINED.
DR EMBL: U01874; AAB18479.1; -
DR EMBL: U20093; AAB19181.1; -
DR EMBL: U19491; AAB19181.1; JOINED.
DR EMBL: M32295; AAA35930.1; ALT_INIT.
DR MIM: 155550; -
DR InterPro: IPR000601; -
DR Pfam: PF00801; PKD; 1.
DR PROSITE: PS50093; PKD; 1.
KW Transmembrane; Glycoprotein; signal; Melanin biosynthesis; Repeat;
KW Antigen.
FT SIGNAL 1 24
FT CHAIN 25 661
FT DOMAIN 25 595
FT TRANSMEM 596 616
FT DOMAIN 617 661
FT DOMAIN 255 292
FT DOMAIN 315 444
FT DOMAIN 315 327
FT REPEAT 328 340
FT REPEAT 341 353
FT REPEAT 354 366
FT REPEAT 367 379
FT REPEAT 380 392
FT REPEAT 393 405
FT REPEAT 406 418
FT REPEAT 419 431
FT REPEAT 432 444
FT REPEAT 445 457
FT CARBOHYD 81 106
FT CARBOHYD 106 111
FT CARBOHYD 111 121
FT CARBOHYD 121 131
FT CARBOHYD 131 141
FT CARBOHYD 141 151
FT CARBOHYD 151 161
FT CARBOHYD 161 171
FT CARBOHYD 171 181
FT CARBOHYD 181 191
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FT CARBOHYD 541 551
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FT  VARIANT      603      626      AAPAGLQVARGLGENSPILSGOV -> SSASINSSRRPWP
RT  MATCHES      7, Conservative 1; Mismatches 1; Indels 0; Gaps 0;
SQ  SEQUENCE     626 AA: 65980 MW: 7AB94ID2E3FB1044 CRC64;

Query Match      84.5%; Score 49; DB 1; Length 626;
Best Local Similarity 77.8%; Pred. NO. 1.3;
Matches 7, Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY      1 KTWGQITWAV 9
        ||||:||||
Db       154 KTWGKRWQV 162

RESULT      3
PIL5_CHICK STANDARD: PRT: 762 AA.
AC      098917;
DT      15-JUL-1998 (Rel. 36, Created)
DT      15-JUL-1998 (Rel. 36, Last sequence update)
DT      01-OCT-2000 (Rel. 40, Last annotation update)
DE      MELANOSOMAL MATRIX PROTEIN 115 KDA PROTEIN PRECURSOR.
GN      MPM115.
OS      Gallus gallus (Chicken).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus.
OX      NCBI_TaxID=9031;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=WHITE LEGHORN; TISSUE=Retinal pigment epithelium;
RX      MEDLINE=92020667; PubMed=1924173;
RA      Mochizuki M., Agata K., Eguchi G.;
RT      "Complete sequence and expression of a cDNA encoding a chicken
RL      115-kDa melanosomal matrix protein.";
RN      Pigment Cell Res. 4:41-47(1991).
[2]
RP      CHARACTERIZATION.
RC      STRAIN=WHITE LEGHORN; TISSUE=Retinal pigment epithelium;
RX      MEDLINE=86311098; PubMed=3409326;
RA      Mochizuki M., Agata K., Kobayashi H., Yamamoto T.S., Eguchi G.;
RT      "Expression of gene coding for a melanosomal matrix protein
RL      transcriptionally regulated in the transdifferentiation of chick
RT      embryo pigmented epithelial cells.";
RN      Cell Differ. 24:67-74(1988).
-1- FUNCTION: MIGHT BE REQUIRED FOR POLYMERIZATION OF MELANIN ONTO THE
CC      CORE STRUCTURE OF MELANOSOMES WITH ENZYMIC FUNCTION OF TYROSINASE.
CC      -1- SUBCELLULAR LOCATION: ON THE FIBROUS MATRIX STRUCTURE OF THE
CC      PREMELANOSOME.
CC      -1- TISSUE SPECIFICITY: SPECIFIC TO PIGMENTED EPITHELIAL CELLS AND
CC      MELANOCYTES. NOT EXPRESSED IN LENS, NEURAL RETINA, BRAIN, HEART,
CC      GIZZARD OR LIVER.
CC      -1- DEVELOPMENTAL STAGE: EXPRESSED DURING THE REDIFFERENTIATION OF
CC      PIGMENTED EPITHELIAL CELLS (PEC).
CC      -1- PFM: GLYCOSYLATED.
CC      -1- SIMILARITY: BELONGS TO THE PMEL-17/NNB FAMILY.
CC      -1- SIMILARITY: CONTAINS 1 PKD DOMAIN.
-----
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-----
EMBL: D88348; BAAL3589.1; -
DR      InterPro; IPR000601; -
DR      Pfam; PF00801; PKD; 1.
DR      PROSITE; PS50093; PKD; 1.
KW      Signal; Glycoprotein; Repeat.
FT      SIGNAL      1      19      POTENTIAL.
FT      CHAIN       20      762      MELANOSOMAL MATRIX PROTEIN 115 KDA

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FT FT DOMAIN 223 323 PROTEIN.
FT FT DOMAIN 441 532 PKD.
FT FT REPEAT 441 464 4 X 20-24 AA APPROXIMATE TANDEM REPEATS.
FT FT REPEAT 465 488 1.
FT FT REPEAT 489 508 2.
FT FT REPEAT 509 532 3.
FT FT CARBOHYD 111 111 4.
FT FT CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 346 346 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 651 651 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 659 659 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 762 AA; 77356 MW; 172CBDB4FDECE7C6 CMC64;

Query Match 75.9%; Score 44; DB 1; Length 762;
Best Local Similarity 75.0%; Pred. No. 8.9;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TWGQYMAV 9
    |||:| |
Db 161 TWGRYMOV 168

RESULT 4
SLEB_BACSU STANDARD; PRT; 305 AA.
ID SLEB_BACSU
AC P50739;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE SPORE-CORTEX-LYTIC ENZYME PRECURSOR.
GN SLEB.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-168;
RX MEDLINE=964277343; PubMed=8830707;
RA Moriyama R., Hattori A., Miyata S., Kudoh S., Makino S.;
RT "A gene (sleB) encoding a spore cortex-lytic enzyme from Bacillus
RT subtilis and response of the enzyme to L-alanine-mediated
RT germination.";
RL J. Bacteriol. 178:6059-6063(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / MABURG;
RX MEDLINE=96349105; PubMed=8760912;
RA Sorokin A.V., Azevedo V., Zumstein E., Galleron N., Ehrlich S.D.,
RA Serror P.;
RT "Sequence analysis of the Bacillus subtilis chromosome region between
RT the serA and kdg loci cloned in a yeast artificial chromosome.";
RL Microbiology 142:2005-2016(1996).
CC -----
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CC -----
DR EMBL: D79978; BA011473.1; -
DR EMBL: L47648; AAC83957.1; -
DR EMBL: Z99115; CAB14209.1; -
DR EMBL: Z99116; CAB14225.1; -
DR Subtilist; BG11439; sleB.
DR InterPro: IPR002477; -
DR Pfam: PF01471; PG_binding_1; 1.
DR Signal.
FT SIGNAL 1 29 POTENTIAL.

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FT CHAIN 30 305 SPORE-CORTEX-LYTIC ENZYME.
SQ SEQUENCE 305 AA; 34001 MW; 9DF1305975F5BE16 CRC64;

Query Match 72.4%; Score 42; DB 1; Length 305;
Best Local Similarity 85.7%; Pred. No. 7.8;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 MCGYNAV 9
111111
DB 67 MCGYNAV 73

RESULT 5
ID CCSA_CHLVU STANDARD; PRT; 315 AA.
AC P56315;

DT 15-JUL-1998 (rel. 36, Created)
DT 15-JUL-1998 (rel. 36, Last sequence update)
DT 15-JUL-1998 (rel. 36, Last annotation update)
DE CYTOCHROME C BIOGENESIS PROTEIN CCSA.

OS Chloroplast.

OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
OC Chlorellaceae; Chlorella.

OX NCBI_TaxID=3077;

RP SEQUENCE FROM N.A.

RC STRAIN-TAM C-27 / TAMIVA;

RA MEDLINE-97303241; PubMed-9159184;

RA Waksugi T., Nagai T., Kapoor M., Sugita M., Ito M., Ito S.,
RA Tsudzuki T., Nakashima K., Tsudzuki T., Suzuki Y., Hamada A., Ohta T.,
RA Inamura A., Yoshinaga K., Sugitara M.;

*Complete nucleotide sequence of the chloroplast genome from the
RT green alga *Chlorella vulgaris*: the existence of genes possibly
involved in chloroplast division*;

RT Proc. Natl. Acad. Sci. U.S.A. 94:5967-5972(1997).

RL -1- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
HEME ATTACHMENT (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCLI/NRFE/CCSA FAMILY.

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CC EMBL: AB001684; BAA57962.1; -

DR InterPro: IPR002541; -

DR Pfam: PF01578; CYTC_asm. 1.

KW Cytochrome c-type biogenesis; Chloroplast.

SQ SEQUENCE 315 AA; 35471 MW; 5020388E94FEAF10 CRC64;

Query Match 72.4%; Score 42; DB 1; Length 315;
Best Local Similarity 62.5%; Pred. No. 8;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGYNA 8
111111
DB 243 KTWGYNA 250

RESULT 6
ID CCSA_ARATH STANDARD; PRT; 328 AA.
AC P56770;

DT 30-MAY-2000 (rel. 39, Created)

DT 30-MAY-2000 (rel. 39, Last sequence update)
DT 01-OCT-2000 (rel. 40, Last annotation update)

DE CYTOCHROME C BIOGENESIS PROTEIN CCSA.

GN CCSA.

OS Arabidopsis thaliana (Mouse-ear cress).

OG Chloroplast.

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;

OC Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RP SEQUENCE FROM N.A.

RC STRAIN-CV. COLUMBIA;

RA MEDLINE-20039611; PubMed-10574454;

RA Sato S., Nakamura Y., Kaneko T., Asamizu E., Tabata S.;

RT "Complete structure of the chloroplast genome of *Arabidopsis*
thaliana".

RT DNA Res. 6:283-290(1999).

RL -1- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
HEME ATTACHMENT (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCLI/NRFE/CCSA FAMILY.

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CC EMBL: AP000423; BAA84436.1; -

DR InterPro: IPR002541; -

DR Pfam: PF01578; CYTC_asm. 1.

KW Cytochrome c-type biogenesis; Chloroplast.

SQ SEQUENCE 328 AA; 37732 MW; C8BD1508E2924D6F CRC64;

Query Match 70.7%; Score 41; DB 1; Length 328;
Best Local Similarity 71.4%; Pred. No. 12;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGYNA 7
111111
DB 255 KTWGYNA 261

RESULT 7
ID YFAO_ECOLI STANDARD; PRT; 549 AA.
AC P76463;

DT 01-OCT-2000 (rel. 40, Created)

DT 01-OCT-2000 (rel. 40, Last sequence update)

DT 01-OCT-2000 (rel. 40, Last annotation update)

DE HYPOTHETICAL 61.5 KDA PROTEIN IN ATOB-GYRA INTERGENIC REGION

DE PRECURSOR.

GN YFAO.

OS Escherichia coli.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia.

OX NCBI_TaxID=562;

RP SEQUENCE FROM N.A.

RC STRAIN-K12 / MG1655;

RA MEDLINE-97426617; PubMed-9278503;

RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.R., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;

"The complete genome sequence of *Escherichia coli* K-12.";

Science 277:1453-1474(1997).

RL

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 CC -----
 DR EMBL; AE000312; AAC75286.1; -.
 DR Ecogene; EG14079; yfao.
 KW Hypothetical protein; Signal.
 FT SIGNAL 1
 FT CHAIN 20 549
 FT SEQUENCE 549 AA; 61475 MW; 72C26716D953C9D1 CRC64;
 QY 3 WGYW 7
 Db 125 WGYW 129
 Query Match 69.0%; Score 40; DB 1; Length 549;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 8
 ID YCDS_ECOLI STANDARD; PRT; 807 AA.
 AC P75907;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE HYPOTHELTICAL 92.2 KDA PROTEIN IN PHOH-CSSG INTERGENIC REGION
 DE PRECURSOR.
 GN YCDS.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdvision; Enterobacteriaceae;
 CC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE=9743617; PubMed=9276503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE=97061202; PubMed=8905232;
 RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizouchi K.,
 RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
 RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
 RA Yano M., Horiiuchi T.;
 RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
 RT corresponding to the 12.7-28.0 min region on the linkage map.";
 RL DNA Res. 3:137-155(1996).
 CC -1- SUBCELLULAR LOCATION: OUTER MEMBRANE (POTENTIAL).
 CC -1- SIMILARITY: STRONG. TO Y. PESTIS HEMIN-BINDING PROTEIN HNSH.
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 CC -----
 DR EMBL; AE000204; AAC74109.1; -.
 DR EMBL; D90739; BAA35806.1; -.
 DR EMBL; D90740; BAA35809.1; -.
 DR Ecogene; EG13865; ycds.

KW Hypothetical protein; Outer membrane; Signal.
 FT SIGNAL 1
 FT CHAIN 27 807
 FT SEQUENCE 807 AA; 92207 MW; B20067C3D41723FD CRC64;
 QY 3 WGYW 7
 Db 314 WGYW 318
 Query Match 69.0%; Score 40; DB 1; Length 807;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 9
 ID FCP_ISOGA STANDARD; PRT; 208 AA.
 AC Q39709;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE FUCOXANTHIN-CHLOROPHYLL A-C BINDING PROTEIN, CHLOROPLAST PRECURSOR
 DE (FCP).
 GN FCP.
 OS Isochrysis galbana.
 OC Eukaryota; Haptophyceae; Isochrysidales; Isochrysis.
 OX NCBI_TaxID=37099;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN-DUN;
 RX MEDLINE=94325461; PubMed=8049362;
 RA Laroche J., Henry D., Wyman K., Suenik A., Falkowski P.;
 RT "Cloning and nucleotide sequence of a cDNA encoding a major
 RT fucoxanthin-chlorophyll a/c-containing protein from the chrysophyte
 RT Isochrysis galbana: implications for evolution of the cab gene
 RT family.";
 RL Plant Mol. Biol. 25:355-368(1994).
 CC -1- FUNCTION: THE LIGHT-HARVESTING COMPLEX (LHC) FUNCTIONS AS A LIGHT
 CC RECEPTOR. IT CAPTURES & DELIVERS EXCITATION ENERGY TO PHOTOSYSTEMS
 CC WITH WHICH IT IS CLOSELY ASSOCIATED. ENERGY IS TRANSFERRED FROM
 CC THE CAROTENOID AND CHL C (OR B) TO CHL A AND THE PHOTOSYNTHETIC
 CC REACTION CENTERS WHERE IT IS USED TO SYNTHESIZE ATP AND REDUCING
 CC POWER.
 CC -1- SUBUNIT: THE LHC COMPLEX OF CHROMOPHYTIC ALGAE IS COMPOSED OF
 CC FUCOXANTHIN, CHLOROPHYLL A AND C BOUND NON-COVALENTLY BY
 CC PIGMENTS IN LHC; FUCOXANTHIN: CHLOROPHYLL C: CHLOROPHYLL A IS
 CC (0.6-1): (0.1-0.3): (1).
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE. FCPs ARE
 CC PROBABLY TRANSPORTED ACROSS THE ENDOPLASMIC RETICULUM MEMBRANE
 CC THAT SURROUND THE PLASTID VIA A SIGNAL PEPTIDE, FOLLOWED BY
 CC TRANSLOCATION ACROSS THE THYLAKOID MEMBRANE VIA A TRANSIT PEPTIDE.
 CC -1- INDUCTION: EXPRESSION IS INCREASED 5-FOLD UNDER CONDITIONS OF
 CC LOW LIGHT.
 CC -1- SIMILARITY: BELONGS TO THE FCP FAMILY OF LIGHT-HARVESTING
 CC PROTEINS.
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 CC -----
 DR EMBL; X77333; CAA54547.1; -.
 DR InterPro; IPR001344; -.
 DR Pfam; PF00504; chloroa_b-bind; 2
 DR Light-harvesting polypeptide; Chloroplast; Photosynthesis;
 KW Photosystem II; Multigene family; Chlorophyll; Transmembrane;
 KW Thylakoid membrane; Transit peptide.
 FT TRANSIT 1 31
 FT CHLOROPLAST (PROBABLE).

FT CHAIN 32 208 FUCOXANTHIN-CHLOROPHYLL A-C BINDING
 FT TRANSMEM 102 118 POTENTIAL.
 SO SEQUENCE 208 AA: 22471 MW: 21A36700137A0F1B CRC64;

Query Match 67.2%; Score 39; DB 1; Length 208;
 Best Local Similarity 83.3%; Pred. No. 16;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TWGOY 7
 DB 198 TWGTFW 203

RESULT 10
 Y090 MYCTU STANDARD; PRT; 256 AA.

AC 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE HYPOTHEICAL 27.8 KDA PROTEIN RV0090.
 GN RV0090 OR MTCY251.08
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
 Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 Oliver S., Osbourne J., Quail M.A., Rajandream M.A., Rogers J.,
 Ruter S., Seeger K., Skelton S., Squares S., Squires R., Sulston J.E.,
 Taylor K., Whitehead S., Barrell B.G.;
 RA "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence."
 RL Nature 393:537-544(1998).

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CC EMBL: Z74410; CAA98926.1; -
 DR Tuberculin: RV0090; -
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 155 175 POTENTIAL.
 FT TRANSMEM 203 223 POTENTIAL.
 SO SEQUENCE 256 AA: 27837 MW: 01033C21199DEC51 CRC64;

Query Match 67.2%; Score 39; DB 1; Length 256;
 Best Local Similarity 66.7%; Pred. No. 19;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGOY 9
 DB 177 KRWGEYFAV 185

RESULT 11
 PTP1_YEAST STANDARD; PRT; 335 AA.
 ID PTP1_YEAST
 AC P25044;

DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE PROTEIN-TYROSINE PHOSPHATASE 1 (EC 3.1.3.48) (PTPase 1).
 GN PTP1 OR YDL230W.

OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=91302312; PubMed=1649172;
 RA Guan K., Deschenes R.J., Qiu H., Dixon J.E.;
 RT "Cloning and expression of a yeast protein tyrosine phosphatase."
 RL J. Biol. Chem. 266:12964-12970(1991).

CC [2]
 CC SEQUENCE FROM N.A.
 RA Rasmussen S.W.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: IS NOT REQUIRED FOR VEGETATIVE GROWTH.
 CC -1- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O =
 CC PROTEIN TYROSINE + ORTHOPHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 CC TYROSINE PHOSPHATASE FAMILY.

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DR EMBL: M64062; AAA34923.1; -
 DR EMBL: Z74278; CAA98809.1; -
 DR PIR: A39862; A39862.
 DR HSP: P18052; 1YFO.
 DR SGD: S0002389; PTP1.
 DR InterPro: IPR000242; -
 DR InterPro: IPR000387; -
 DR Pfam: PF00102; Y-phosphatase; 1.
 DR PRINTS: PR00700; PRYPHPTASE.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
 KW Hydrolase.
 FT ACT_SITE 252 252 BY SIMILARITY.
 SO SEQUENCE 335 AA: 38868 MW: 15F71E50694BE562 CRC64;

Query Match 67.2%; Score 39; DB 1; Length 335;
 Best Local Similarity 71.4%; Pred. No. 24;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGOY 7
 DB 108 KTWQDFW 114

RESULT 12
 PTP2B_ARATH STANDARD; PRT; 585 AA.
 ID PTP2B_ARATH
 AC P46032;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE PEPTIDE TRANSPORTER PTP2-B (HISTIDINE TRANSPORTING PROTEIN).
 GN PTP2-B OR NTR1 OR AT2G02040 OR F14H20.11.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;
 RN [1]
 RC SEQUENCE FROM N.A.
 RA STRAIN=CV, LANDSBERG ERECTA;
 RA Song W., Steiner H.-Y., Zhang L., Naider F., Stacey G.,
 RA Becker J.M.;
 RL Submitted (xxx-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, C24;
 RA MEDLINE=94307379; PubMed=8033999;
 RA Frommer W.B., Hummel S., Rentsch D.;
 RT "Cloning of an Arabidopsis histidine transporting protein related to
 RT nitrate and peptide transporters.";
 RL FEMS Lett. 347:185-189(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, COLUMBIA;
 RA MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
 RA Cronin L.A., Shen M., Vanden S.E., Umayam L., Tallon L.J., Gill J.E.,
 RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
 RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
 RA Salzberg S.L., Fraser C.M., Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 RT thaliana.";
 RL Nature 402:761-768(1999).
 CC -1- FUNCTION: PEPTIDE TRANSPORT. HIGH AFFINITY, LOW CAPACITY
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE PPR2 FAMILY OF TRANSPORTERS.
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 DR EMBL: L39082; AAB00858.1; -;
 DR EMBL: X77503; CA54634.1; -;
 DR EMBL: AC006532; AAD20096.1; -;
 DR InterPro: IPR000109; -;
 DR Pfam: PF00854; PTR2.1;
 DR PROSITE: PS01022; PTR2.1; 1;
 DR PROSITE: PS01023; PTR2.2; 1;
 KW Peptide transport; Transport; Transmembrane.
 FT TRANSMEM 91 111 POTENTIAL.
 FT TRANSMEM 116 136 POTENTIAL.
 FT TRANSMEM 154 174 POTENTIAL.
 FT TRANSMEM 200 220 POTENTIAL.
 FT TRANSMEM 228 248 POTENTIAL.
 FT TRANSMEM 351 371 POTENTIAL.
 FT TRANSMEM 387 407 POTENTIAL.
 FT TRANSMEM 431 451 POTENTIAL.
 FT TRANSMEM 472 492 POTENTIAL.
 FT TRANSMEM 511 531 POTENTIAL.
 FT TRANSMEM 556 576 POTENTIAL.
 FT CONFLICT 334 334 R -> ED (IN REF. 2).
 SQ SEQUENCE 585 AA; 64421 MM; C58F8194776E2D97 CMC64;

QY 3 WGVYAV 9
 DB 110 WGRWTI 116
 Query Match 67.2%; Score 39; DB 1; Length 585;
 Best Local Similarity 57.1%; Pred. No. 40;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 13
 ID CYST_ECOLI STANDARD; PRT; 277 AA.
 AC P16701;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE SULFATE TRANSPORT SYSTEM PERMEASE PROTEIN CYST.
 GN CYSU OR CYST.
 OS Escherichia coli.
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RA MEDLINE=90264334; PubMed=2188958;
 RA Sirko A., Hryniewicz M.M., Hulanicka D.M., Boeck A.;
 RT "Sulfate and thiosulfate transport in Escherichia coli K-12:
 RT nucleotide sequence and expression of the cystWAM gene cluster.";
 RL J. Bacteriol. 172:3351-3357(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RA MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RA MEDLINE=97349980; PubMed=9205837;
 RA Yanamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K.,
 RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
 RA Mizobuchi K., Mori H., Nakada S., Nakamura Y., Nishimoto H.,
 RA Oshima T., Oyama S., Saito N., Sempel G., Satoh Y., Sivasubram S.,
 RA Yamagata H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
 RA Yamaguchi T.;
 RT "Construction of a contiguous 874-kb sequence of the Escherichia coli
 RT K-12 genome corresponding to 50.0-68.8 min on the linkage map and
 RT analysis of its sequence features.";
 RL DNA Res. 4:91-113(1997).
 CC -1- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
 CC FOR SULFATE AND THIOSULFATE. PROBABLY RESPONSIBLE FOR THE
 CC TRANSLLOCATION OF THE SUBSTRATE ACROSS THE MEMBRANE.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
 CC (POTENTIAL).
 CC -1- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
 CC PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE CYSTW
 CC SUBFAMILY.
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 DR EMBL: M32101; AAA23637.1; -;
 DR EMBL: AE000330; AAC75477.1; -;
 DR EMBL: D90871; BAA16298.1; -;
 DR EMBL: D90872; BAA16307.1; -;
 DR PIR: A35402; QRECSF.
 DR PIR: B35403; B35403.
 DR EcGene: BG10197; cySU.
 DR InterPro: IPR000515; -;
 DR Pfam: PF00528; BPD_transp.1.
 DR PROSITE: PS00402; BPD_transp_inn_membr.1.

KW Inner membrane; Transmembrane; Sulfate transport; Transport.
 FT TRANSMEM 21 39 POTENTIAL.
 FT TRANSMEM 64 80 POTENTIAL.
 FT TRANSMEM 105 121 POTENTIAL.
 FT TRANSMEM 140 156 POTENTIAL.
 FT TRANSMEM 188 204 POTENTIAL.
 FT TRANSMEM 247 259 POTENTIAL.
 SQ SEQUENCE 277 AA; 30291 MW; 1342821B0DE24459 CRC64.

Query Match 65.5%; Score 38; DB 1; Length 277;
 Best Local Similarity 62.5%; Pred. No. 29;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 TWGQYAV 9
 DB 43 SNAQYMEV 50

RESULT 14
 ID UBIA.ECOLI STANDARD; PRT; 290 AA.
 AC P26601;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE 4-HYDROXYBENZATE OCTAPRENYLTRANSFERASE (EC 2.5.1.-) (4-HB
 DE POLYPRENYLTRANSFERASE).
 GN UBIA OR CYR.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE-92355505; PubMed1644758;
 RA Nichols B.P., Green J.M.;
 RT "Cloning and sequencing of Escherichia coli ublc and purification of
 RT chorismate lyase.";
 RL J. Bacteriol. 174:5309-5316(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MC4100;
 RX MEDLINE-92354744; PubMed-1644192;
 RA Siebert M., Bechtold A., Weizer M., May U., Berger U., Schroeder G.,
 RT "Ubiquinone biosynthesis. Cloning of the genes coding for chorismate
 RT pyruvate-lyase and 4-hydroxybenzoate octaprenyl transferase from
 RT Escherichia coli.";
 RL FEBS Lett. 307:347-350(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / W3110;
 RX MEDLINE-92380960; PubMed-151213;
 RA Nishimura K., Nakahigashi K., Inokuchi H.;
 RT "Location of the ubla gene on the physical map of Escherichia coli.";
 RL J. Bacteriol. 174:5762-5762(1992).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RA Wolter F.P.;
 RL Submitted (NOV-1992) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE-94089392; PubMed-8265357;
 RA Blatner F.R., Burland V.D., Plunkett G. III, Sofia H.J.,
 RA Daniels D.L.;
 RT "Analysis of the Escherichia coli genome. IV. DNA sequence of the
 RT region from 89.2 to 92.8 minutes.";
 RL Nucleic Acids Res. 21:5408-5417(1993).
 RN [6]

RP SEQUENCE OF 1-80 FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE-94014977; PubMed-8409922;
 RA Wu G., Williams H.D., Gibson F., Poole R.K.;
 RT "Mutants of Escherichia coli affected in respiration: the cloning and
 RT nucleotide sequence of ubla, encoding the membrane-bound p-
 RT hydroxybenzoate:octaprenyltransferase.";
 RL J. Gen. Microbiol. 139:1795-1805(1993).
 RN [7]
 RP CHARACTERIZATION.
 RX MEDLINE-94207029; PubMed-8155731;
 RA Weller M., Heide L.;
 RT "Characterization of poly(prenyl)phosphate:4-hydroxybenzoate
 RT poly(prenyl)transferase from Escherichia coli.";
 RL Biochim. Biophys. Acta 1212:93-102(1994).
 RN [8]
 RP CHARACTERIZATION.
 RX MEDLINE-95072311; PubMed-7765507;
 RA Suzuki K., Ueda M., Yuasa M., Nakagawa T., Kawamukai M., Matsuda H.;
 RT "Evidence that Escherichia coli ubla product is a functional homolog
 RT of yeast COO2, and the regulation of ubla gene expression.";
 RL Biosci. Biotechnol. Biochem. 58:1814-1819(1994).
 CC -1- FUNCTION: SYNTHESIS OF 3-OCTAPRENYL-4-HYDROXYBENZATE.
 CC -1- CATALYTIC ACTIVITY: 4-HYDROXYBENZATE + FARNESYLFARNESYLGERANIOL
 CC -1- COFACTOR: REQUIRES MAGNESIUM.
 CC -1- PATHWAY: SECOND STEP IN UBIQUINONE BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
 CC -1- SIMILARITY: BELONGS TO THE UBIA PRENYLTRANSFERASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; M93136; AAA24712.1; -
 DR EMBL; M93413; AAA24717.1; -
 DR EMBL; X66619; CAA47182.1; -
 DR EMBL; X57434; CAA40682.1; -
 DR EMBL; X69522; CAA49270.1; -
 DR EMBL; U00006; AAC43134.1; -
 DR EMBL; AE000477; AAC77010.1; -
 DR EMBL; M96268; AAA17028.1; -
 DR EMBL; X63407; CAA45003.1; -
 DR PIR; BA2956; B42956.
 DR PIR; S24361; S24361.
 DR PIR; S25661; S25661.
 DR PIR; S31432; S31432.
 DR PIR; JC2316; JC2316.
 DR Ecogen; EG11370; ubla.
 DR InterPro; IPR000537; -
 DR Pfam; PF01040; UBIA.1.
 DR PROSITE; PS00943; UBIA.1.
 KW Ubiquinone biosynthesis; Transferase; Transmembrane; Inner membrane;
 KW Magnesium.
 FT TRANSMEM 23 43 POTENTIAL.
 FT TRANSMEM 46 66 POTENTIAL.
 FT TRANSMEM 100 120 POTENTIAL.
 FT TRANSMEM 141 161 POTENTIAL.
 FT TRANSMEM 163 183 POTENTIAL.
 FT TRANSMEM 213 233 POTENTIAL.
 FT TRANSMEM 234 254 POTENTIAL.
 FT TRANSMEM 268 288 POTENTIAL.
 SQ SEQUENCE 290 AA; 32511 MW; F10FED1DA30E115 CRC64;

Query Match 65.5%; Score 38; DB 1; Length 290;
 Best Local Similarity 57.1%; Pred. No. 30;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 WGOYMAV 9
1111:
Db 237 WGOYMSI 243

RESULT 15
XVNC_STRLI STANDARD: PRT: 240 AA.
AC P26220:
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENDO-1,4-BETA-XYLANASE C PRECURSOR (EC 3.2.1.8) (XYLANASE C)
DE (1,4-BETA-D-XYLAN XYLANOXYDROLASE C).
GN XINC.
OS Streptomyces lividans.
OC Bacteria; Filicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1916;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 50-80.
RC STRAIN=66 / 1326;
RX MEDLINE=92077439; PubMed=1743521;
RA Sharek F., Roy C., Yaguchi M., Morosoli R., Kluepfel D.;
RT "Sequences of three genes specifying xylanases in Streptomyces
RT lividans.";
RL Gene 107:75-82(1991).
CC -1- FUNCTION: CONTRIBUTES TO HYDROLASE HEMICELLULOSE. THE MAJOR
CC COMPONENT OF PLANT CELL-WALLS.
CC -1- CATALYTIC ACTIVITY: ENDOMYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
CC LINKAGES IN XYLANS.
CC -1- PATHWAY: XYLAN DEGRADATION.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
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CC -----
DR EMBL: M64553; AAA26836.1; -;
DR EMBL: A25307; CAA01768.1; -;
DR PIR: JS0591; JS0591.
DR HSSP: P09850; IBCX.
DR InterPro: IPR001137; -;
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE1.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Xylan degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 49
FT CHAIN 50 240 ENDO-1,4-BETA-XYLANASE C.
FT ACCT_SITE 134 134 NUCLEOPHILE (BY SIMILARITY).
FT ACCT_SITE 226 226 PROTON DONOR (BY SIMILARITY).
FT SEQUENCE 240 AA; 23673 MW; FC663415780142CA CRC64;
SQ

Query Match 63.8%; Score 37; DB 1; Length 240;
Best Local Similarity 66.7%; Pred. No. 36;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTWGOYMAV 9
1111:
Db 178 KTFQOYMSV 186

RESULT 16
CCSA_CYACA STANDARD: PRT: 306 AA.
ID CCSA_CYACA

P31564;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CYTOCHROME C BIOGENESIS PROTEIN CCSA.
GN CCSA.
OS Cyanidium caldarium (Caldieria sulphuraria).
OG Chloroplast.
OC Eukaryota; Rhodophyta; Bangiophyceae; Porphyridiales; Porphyridiaceae;
OC Cyanidium.
OX NCBI_TaxID=2771;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=14-1-1 / ISOLATE 107 79/GOETTINGEN;
RX MEDLINE=93004479; PubMed=1391770;
RA Valentin K., Maid U., Emich A., Zetsche K.;
RT "Organization and expression of a phycoobiliprotein gene cluster from
RT the unicellular red alga Cyanidium caldarium.";
RL Plant Mol. Biol. 20:267-276(1992).
CC -1- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
CC HEME ATTACHMENT (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL/NRPF/CCSA FAMILY.
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CC -----
DR EMBL: X57150; CAA0439.1; -;
DR PIR: S14520; S14520.
DR PIR: S25309; S25309.
DR InterPro: IPR002541; -;
DR Pfam: PF01578; CytC_asm; 1.
KW Cytochrome c-type biogenesis; Chloroplast.
SQ SEQUENCE 306 AA; 35263 MW; 4C3C9AFB48292F4F CRC64;
SQ

Query Match 63.8%; Score 37; DB 1; Length 306;
Best Local Similarity 50.0%; Pred. No. 45;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 17
CCSA_ODOSI STANDARD: PRT: 312 AA.
AC P49523;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CYTOCHROME C BIOGENESIS PROTEIN CCSA.
GN CCSA.
OS Odontella sinensis.
OG Chloroplast.
OC Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;
OC Biddulphiophycidae; Eupodiscales; Eupodisaceae; Odontella.
OX NCBI_TaxID=2839;
RN [1]
RP SEQUENCE FROM N.A.
RA Kowalik K.V., Stoebe B., Schaffran I., Kroth-Pancic P., Freier U.;
RT "The chloroplast genome of a chlorophyll a+c-containing alga,
RT Odontella sinensis.";
RL Plant Mol. Biol. Rep. 13:336-342(1995).
CC -1- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
CC HEME ATTACHMENT (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL/NRPF/CCSA FAMILY.
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DR EMBL: Z67753; CAA91615.1; -
 DR InterPro: IPR002541; -
 DR Pfam: PF01578; CytC_asm.1;
 KW Cytochrome c-type biogenesis; Chloroplast.
 SQ SEQUENCE 312 AA; 35436 MW; 748390BE4BE3C5B9 CRC64;

Query Match 63.8%; Score 37; DB 1; Length 312;

Best Local Similarity 50.0%; Pred. No. 46; Mismatches 2; Indels 0; Gaps 0;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTWGQYWA 8
 DB 241 EAMGSYMS 248

RESULT 18
 MANA_STRMU STANDARD; PRT; 316 AA.
 AC 059935;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8) (PHOSPHOMANNOSE ISOMERASE)
 DE (PMT) (PHOSPHOHEXOMUTASE).
 GN PMT.
 OS Streptococcus mutans.
 CC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 CC Streptococcus
 CC NCB1_TaxID=1309;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN-GS-5;
 RX MEDLINE=94123951; PubMed=8293960;
 RA Sato Y., Yamamoto Y., Kizaki H., Kuramitsu H.K.;
 RT "Isolation and sequence analysis of the pm1 gene encoding
 RT phosphomannose isomerase of Streptococcus mutans."
 RL FEMS Microbiol. Lett. 114:61-66(1993).
 CC -1- CATALYTIC ACTIVITY: D-MANNOSE 6-PHOSPHATE = D-FRUCTOSE
 CC 6-PHOSPHATE.
 CC -1- COFACTOR: ZINC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF MANNOSE-6-PHOSPHATE ISOMERASES.
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DR EMBL: D16594; BAA04021.1; -
 DR InterPro: IPR001250; -
 DR Pfam: PF01238; PM1_Type1; 1.
 DR PROSITE: PS00965; PM1_1; FALSE_NEG.
 DR PROSITE: PS00966; PM1_1_2; FALSE_NEG.
 KN Isomerase; Zinc.
 FT METAL 97 97 ZINC (BY SIMILARITY).
 FT METAL 109 109 ZINC (BY SIMILARITY).
 FT METAL 171 171 ZINC (BY SIMILARITY).
 SQ SEQUENCE 316 AA; 35388 MW; 8FA7B248791BB96A CRC64;

Query Match 63.8%; Score 37; DB 1; Length 316;
 Best Local Similarity 55.6%; Pred. No. 46;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTWGQYWA 9
 DB 32 ETTGETYWA 40

RESULT 19
 CCSA_PORPU STANDARD; PRT; 319 AA.
 ID CCSA_PORPU
 AC P51369; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE CYTOCHROME C BIOGENESIS PROTEIN CCSA.
 GN CCSA.
 OS Porphyra purpurea.
 CC Chloroplast.
 CC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
 CC NCB1_TaxID=2787;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN-AVONPORT;
 RA Reith M.E., Munholland J.;
 RT "Complete nucleotide sequence of the Porphyra purpurea chloroplast
 RT genome."
 RL Plant Mol. Biol. Rep. 13:333-335(1995).
 CC -1- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
 CC HEME ATTACHMENT (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCIL/NRFE/CCSA FAMILY.
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DR EMBL: U38804; AAC08255.1; -
 DR InterPro: IPR002541; -
 DR Pfam: PF01578; CytC_asm.1;
 KW Cytochrome c-type biogenesis; Chloroplast.
 SQ SEQUENCE 319 AA; 35213 MW; 71AFBA3A1B7E0D48 CRC64;

Query Match 63.8%; Score 37; DB 1; Length 319;

Best Local Similarity 50.0%; Pred. No. 47; Mismatches 2; Indels 0; Gaps 0;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTWGQYWA 8
 DB 248 EAMGSYMS 255

RESULT 20
 CCSA_PINTH STANDARD; PRT; 320 AA.
 ID CCSA_PINTH
 AC P41650;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE CYTOCHROME C BIOGENESIS PROTEIN CCSA.
 GN CCSA.
 OS Pinus thunbergii (Green pine) (Japanese black pine).
 CC Chloroplast.
 CC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 CC Coniferopsida; Coniferales; Pinaceae; Pinus.
 CC NCB1_TaxID=3350;
 RN [1]
 RC SEQUENCE FROM N.A.
 RX MEDLINE=95024047; PubMed=7937893;
 RA Wakasugi T., Tsudzuki J., Ito S., Nakashima K., Tsudzuki T.,

RA Sugiura M.;
 RT "Loss of all ndh genes as determined by sequencing the entire
 RT chloroplast genome of the black pine *Pinus thunbergii*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:9794-9798(1994).
 CC -1- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
 CC HEME ATTACHMENT (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL1/NRFE/CCSA FAMILY.
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 CC -----
 CC EMBL: D17510; BAA04448.1; -;
 CC InterPro: IPR002541; -;
 CC Pfam: PF01578; Cytc_asm; 1.
 CC Cytochrome c-type biogenesis; Chloroplast.
 KW SEQUENCE 320 AA; 36262 MW; 12D641127F4B306E CRC64;
 SQ
 Query Match 63.8%; Score 37; DB 1; Length 320;
 Best Local Similarity 50.0%; Pred. No. 47;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 KTWGQYMA 8
 Db 248 EAWGSYWS 255
 RESULT 21
 ID CCSA_CYAPA STANDARD; PRT; 322 AA.
 AC P48257;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE CYTOCHROME C BIOGENESIS PROTEIN CCSA.
 GN CCSA.
 OS Cyanophora paradoxa.
 OG Cyanelle.
 OC Eukaryota; Glaucocystophyceae; Cyanophoraceae; Cyanophora.
 OX NCBI_Taxid=2762;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LB555 / PRINGSHEIM;
 RA Striwall V.L., Michalowski C.B., Luffelhardt W., Bohnert H.J.,
 RA Bryant D.A.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
 CC HEME ATTACHMENT (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL1/NRFE/CCSA FAMILY.
 CC -----
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 CC -----
 CC EMBL: U30821; AAA81298.1; -;
 CC InterPro: IPR002541; -;
 CC Pfam: PF01578; Cytc_asm; 1.
 CC Cytochrome c-type biogenesis; Cyanelle.
 KW SEQUENCE 322 AA; 37453 MW; 7E0CB2E5012A1838 CRC64;
 SQ
 Query Match 63.8%; Score 37; DB 1; Length 322;
 Best Local Similarity 50.0%; Pred. No. 47;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 KTWGQYMA 8
 Db 251 EAWGSYWS 258
 RESULT 22
 ID CCSA_CHLRE STANDARD; PRT; 353 AA.
 AC P48269;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE CYTOCHROME C BIOGENESIS PROTEIN CCSA.
 GN CCSA.
 OS Chlamydomonas reinhardtii.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 CC Chlamydomonadaceae; Chlamydomonas.
 OX NCBI_Taxid=3055;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CC-400;
 RC MEDLINE=95334509; PubMed=7610180;
 RA Chen Z.Y., Moroney J.V.;
 RT "Identification of a Chlamydomonas reinhardtii chloroplast gene with
 RT significant homology to bacterial genes involved in cytochrome c
 RT biosynthesis.";
 RL Plant Physiol. 108:843-844(1995).
 RN [2]
 RP SEQUENCE FROM N.A., AND FUNCTION.
 RC STRAIN=CC-503;
 RC MEDLINE=96214878; PubMed=8617725;
 RA Xie Z., Merchant S.;
 RT "The plastid-encoded *ccsa* gene is required for heme attachment to
 RT chloroplast c-type cytochromes.";
 RL J. Biol. Chem. 271:4632-4639(1996).
 CC -1- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
 CC HEME ATTACHMENT.
 CC -1- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL1/NRFE/CCSA FAMILY.
 CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-20 IS THE INITIATOR.
 CC -----
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 CC -----
 CC EMBL: U15556; AAA76600.1; -;
 CC InterPro: IPR002541; -;
 CC Pfam: PF01578; Cytc_asm; 1.
 CC Cytochrome c-type biogenesis; Chloroplast.
 KW COMPACT 342 342 T->I (IN REF. 2).
 FT SEQUENCE 353 AA; 39971 MW; 3D46ABC578044C4B CRC64;
 SQ
 Query Match 63.8%; Score 37; DB 1; Length 353;
 Best Local Similarity 50.0%; Pred. No. 51;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 KTWGQYMA 8
 Db 282 EAWGSYWS 289
 RESULT 23
 ID SMF_HAEIN STANDARD; PRT; 373 AA.
 AC P43862;
 DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, last sequence update)
 DT 15-DEC-1998 (Rel. 37, last annotation update)
 DE SMF PROTEIN (DNA PROCESSING CHAIN A).
 GN SMF OR DPRA OR H10985.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellales;
 OC Haemophilus.
 OX NCBI_Taxid=727;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-RD / KM20 / ATCC 51907;
 RA Karandapuram S., Zhao X., Barcak G.J.;
 RL Submitted (Dec-1994) to the EMBL/Genbank/DBJ databases.
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN-RD / KM20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 Kerlavage A.R., Sutton G., Fritch J.W., Fields C.A., Gocayne J.D.,
 McKenney K., Sutton G., Fritch J.W., Fields C.A., Gocayne J.D.,
 Scott J.D., Shiley R., Liu L.-I., Glodex A., Kelley J.M.,
 Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 Fine L.D., Fritchman J.L., Fuhrman J.L., Geoghegan N.S.M.,
 Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 Venter J.C.;
 RA "Whole-genome random sequencing and assembly of Haemophilus
 influenzae Rd.";
 RT Science 269:496-512(1995).
 CC -1- FUNCTION: REQUIRED FOR CHROMOSOMAL BUT NOT PLASMID TRANSFORMATION.
 CC -1- SIMILARITY: BELONGS TO THE SMF FAMILY.
 CC -----
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 CC -----
 DR EMBL: U18657; AAA7011.1; -
 DR EMBL: U32779; AAC22646.1; -
 DR TIGR: H10985; -
 SO SEQUENCE 373 AA; 41633 MW; 26E0353372EF61F CRC64;

Query Match 63.8%; Score 37; DB 1; Length 373;
 Best Local Similarity 71.4%; Pred. No. 54;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 TWGQYWA 8
 DB 123 TYGEYWA 129

RESULT 24
 YG10_ECOLI STANDARD; PRT; 739 AA.
 AC 046861; Q46862;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE HYPOTHETICAL 83.5 KDA PROTEIN IN METC-SUPI INTERGENIC REGION.
 GN YG10 OR B3015/B3016.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_Taxid=562;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,

RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN (2)
 RP CONCEPTUAL TRANSLATION.
 RA Rudd K.E.;
 RL Unpublished observations (JUN-1999).
 CC -1- SIMILARITY: TO M. JANNASCHIT MJ1155. ALSO SOME SIMILARITY TO FAMILY
 CC UPF0004.
 CC -1- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A FRAMESHIFT WAS
 CC INTRODUCED IN POSITION 319 TO PRODUCE THIS ORF.
 CC -----
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 CC -----
 DR EMBL: U28377; AAA69183.1; ALT_FRAME.
 DR EMBL: U28377; AAA69184.1; ALT_FRAME.
 DR EMBL: AE000383; AAC76052.1; ALT_FRAME.
 DR EMBL: AE000383; AAC76051.1; ALT_FRAME.
 DR Ecocore: E013019; Y910.
 KW Hypothetical protein.
 SO SEQUENCE 739 AA; 83503 MW; ECE565EC891584A CRC64;

Query Match 63.8%; Score 37; DB 1; Length 739;
 Best Local Similarity 71.4%; Pred. No. 1e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 TWGQYWA 8
 DB 15 SMPQYWA 21

RESULT 25
 XYND_RUMFL STANDARD; PRT; 802 AA.
 AC 053317;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE XYLANASE/BETA-GLUCANASE PRECURSOR [INCLUDES: ENDO-1,4-BETA-XYLANASE
 DE (EC 3.2.1.8) (XYLANASE); (ENDO-BETA-1,3-1,4 GLUCANASE) (EC 3.2.1.73)
 DE (1,3-1,4-BETA-D-GLUCAN 4-GLUCANOHYDROLASE) (LICHENASE)].
 GN XYND.
 OS Ruminococcus flavefaciens.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
 OC Ruminococcus.
 OX NCBI_Taxid=1265;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-17;
 RX MEDLINE=93259938; PubMed=8491715;
 RA Flint H.J., Martin J., McPherson C.A., Daniel A.S., Zhang J.-X.;
 RT "A bifunctional enzyme, with separate xylanase and beta(1,3-1,4)-
 RT glucanase domains, encoded by the xynD gene of Ruminococcus
 RT flavefaciens.";
 RL J. Bacteriol. 175:2943-2951(1993).
 CC -1- FUNCTION: CONTAINS TWO CATALYTIC DOMAINS WITH XYLANASE AND ENDO-
 CC BETA-1,3-1,4 GLUCANASE ACTIVITIES.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
 CC LINKAGES IN XYLANS.
 CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF 1,4-BETA-D-GLYCOSIDIC LINKAGES
 CC IN BETA-D-GLUCANS CONTAINING 1,3- AND 1,4-BONDS.
 CC -1- PATHWAY: XYLAN DEGRADATION.
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO CELLULOSE FAMILY
 CC 6 (FAMILY 11 OF GLYCOSYL HYDROLASES).

CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO FAMILY 16 OF
CC GLYCOSYL HYDROLASES.
CC
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CC
DR EMBL; S61204; AAB26620.1; -
DR HSSP; P23904; 1AJX.
DR InterPro; IPR000757; -
DR InterPro; IPR001137; -
DR Pfam; PF02018; CBD_6; 1.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR Pfam; PF00722; Glyco_hydro_16; 1.
DR PRINTS; PR00737; GLHYDRLASE1.
DR PRINTS; PR00911; GLHYDRLASE1.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.
DR Xylan degradation; Hydrolase; Glycosidase; Signal;
KM Multifunctional enzyme.
FT SIGNAL 1 31
FT CHAIN 32 802
FT DOMAIN 32 244
FT DOMAIN 245 523
FT DOMAIN 524 555
FT DOMAIN 556 802
FT ACT_SITE 124 124
FT ACT_SITE 226 226
FT ACT_SITE 684 684
FT DOMAIN 524 529
FT DOMAIN 532 543
FT DOMAIN 546 553
SQ SEQUENCE 802 AA; 89091 MW; 2880A689647284AF CRC64;

Query Match 63.88; Score 37; DB 1; Length 802;
Best Local Similarity 66.7%; Pred. No. 1.le+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGYMAY 9
DB 172 KTFPTWMSV 180

RESULT 26
YE68_METJA STANDARD; PRT; 1009 AA.
ID YE68_METJA
AC 058863;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE HYPOTHETICAL PROTEIN MJ1468.
GN MJ1468.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 2661;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake O., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weissstock K.G., Herrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uitterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

RA Klenk H.-P., Fraser C.M., Smith H.O., Moese C.R., Venter J.C.;
RT "complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.";
RL Science 273:1058-1073(1996).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: CONTAINS 5 PKD DOMAINS.
CC
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CC
DR EMBL; U67588; AAB99478.1; -
DR TIGR; MJ1468; -
DR InterPro; IPR000601; -
DR Pfam; PF00801; PKD; 3.
DR PROSITE; PS50093; PKD; 5.
KM Hypothetical protein; Transmembrane; Repeat.
FT TRANSMEM 6 26
FT TRANSMEM 985 1005
FT DOMAIN 213 247
FT DOMAIN 436 503
FT DOMAIN 724 806
FT DOMAIN 822 886
FT DOMAIN 925 962
FT DOMAIN 293 298
SQ SEQUENCE 1009 AA; 115119 MW; 13E9B4933EAB7972 CRC64;

Query Match 63.88; Score 37; DB 1; Length 1009;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 WGYMAY 7
DB 322 WGYMAY 326

RESULT 27
PA21_BUNMU STANDARD; PRT; 120 AA.
ID PA21_BUNMU
AC P00617;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PHOSPHOLIPASE A2, BETA BUNGAROTOXIN A1 CHAIN (EC 3.1.1.4)
DE (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE).
OS Bungarus multicinctus (Many-banded krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Bungarinae; Bungarus.
OX NCBI_TaxID=8616;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=78109400; PubMed=624701;
RA Kondo K., Narita K., Lee C.-Y.;
RT "Amino acid sequences of the two polypeptide chains in beta-1-
RT bungarotoxin from the venom of Bungarus multicinctus.";
RL J. Biochem. 83:101-115(1978).
RN [2]
RP SEQUENCE, AND REVISIONS TO 85-87 AND 109.
RX MEDLINE=82239269; PubMed=7096304;
RA Kondo K., Toda H., Narita K., Lee C.-Y.;
RT "Amino acid sequence of beta 2-bungarotoxin from Bungarus
RT multicinctus venom. The amino acid substitutions in the B chains.";
RL J. Biochem. 91:1519-1530(1982).
RN [3]
RP CHARACTERIZATION OF PHOSPHOLIPASE A2 ACTIVITY.
RX MEDLINE=79088714; PubMed=730754;

RA Kondo K., Toda H., Narita K.;
RT "Characterization of phospholipase A activity of beta1-bungarotoxin
from Bungarus multicinctus venom. II. Identification of the histidine
residue of beta1-bungarotoxin modified by p-bromophenacyl bromide.";
RL J. Biochem. 84:1301-1308(1978).
[4]
RN CHARACTERIZATION OF PRESYNAPTIC NEUROTOXINS.
RX MEDLINE-78043174; PubMed-303565;
RA Abe T., Alema S., Miledi R.;
RT "Isolation and characterization of presynaptically acting neurotoxins
from the venom of Bungarus snakes.";
RL Eur. J. Biochem. 80:1-12(1977).
CC -1- FUNCTION: INHIBITS NEUROMUSCULAR TRANSMISSION BY BLOCKING
ACETYLCHOLINE RELEASE FROM THE NERVE TERMINI. ACT PRESYNAPTICALLY.
CC -1- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE
2-ACYL GROUPS IN 3-SN-PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O = 1-ACYLGLYCEROL-
PHOSPHOCHOLINE + A FATTY ACID ANION.
CC -1- SUBUNIT: DIMER OF DISSIMILAR CHAINS LINKED BY ONE OR MORE
DISULFIDE BONDS. THE A CHAINS HAVE PHOSPHOLIPASE A2 ACTIVITY AND
THE B CHAINS SHOW HOMOLOGU WITH THE BASIC PROTEASE INHIBITORS. THE
A1 CHAIN IS FOUND IN BETA-1 AND BETA-2 BUNGAROTOXINS.
CC -1- MISCELLANEOUS: LD(50) IS 0.019 MG/KG BY INTRAPERITONEAL INJECTION
IN BETA-1 BUNGAROTOXIN AND 0.028 MG/KG IN BETA-2.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
DR PIR: A00757; PSKFAU.
DR HSSP: P15445; 1A3F.
DR InterPro: IPR001211; .
DR Pfam: PF00068; phoslip; 1.
DR PRINTS: PR00389; PHPLIPASEA2.
DR PROSITE: PS00118; PA2_HIS; 1.
DR PROSITE: PS00119; PA2_ASP; 1.
KW Hydrolyase; Lipid degradation; Calcium; Multigene family; Venom;
KM Presynaptic neurotoxin.
FT ACT_SITE 48 48 BY SIMILARITY.
FT ACT_SITE 94 94 BY SIMILARITY.
FT DISULFID 15 15 INTERCHAIN (WITH A B CHAIN) (PROBABLE).
FT DISULFID 27 119 BY SIMILARITY.
FT DISULFID 29 45 BY SIMILARITY.
FT DISULFID 44 100 BY SIMILARITY.
FT DISULFID 51 93 BY SIMILARITY.
FT DISULFID 61 86 BY SIMILARITY.
FT DISULFID 79 91 BY SIMILARITY.
FT CA_BIND 49 49 BY SIMILARITY.
FT VARIANT 89 89 I -> V (IN 20%).
SQ SEQUENCE 120 AA; 13489 MW; C6G544CE62CA12C2 CRC64;

Query Match 62.1%; Score 36; DB 1; Length 120;
Best Local Similarity 83.3%; Pred. No. 27;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KTWGOY 6
ID PA22_BUNMU STANDARD; PRT; 120 AA.
AC P00619;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PHOSPHOLIPASE A2, BETA BUNGAROTOXIN A3 CHAIN (EC 3.1.1.4)
(PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE).
OS Bungarus multicinctus (Many-banded Krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylidae; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Bungarinae; Bungarus.
OX NCBI_TaxID=8616;
RN [1]
RP SEQUENCE.

RC TISSUE-Venom;
RX MEDLINE-82239270; PubMed-7096305;
RA Kondo K., Toda H., Narita K., Lee C.-Y.;
RT "Amino acid sequences of three beta-bungarotoxins (beta 3-, beta 4-,
and beta 5-bungarotoxins) from Bungarus multicinctus venom. Amino
acid substitutions in the A chains.";
RL J. Biochem. 91:1531-1548(1982).
CC -1- FUNCTION: INHIBITS NEUROMUSCULAR TRANSMISSION BY BLOCKING
ACETYLCHOLINE RELEASE FROM THE NERVE TERMINI. ACT PRESYNAPTICALLY.
CC -1- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE
2-ACYL GROUPS IN 3-SN-PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O = 1-ACYLGLYCEROL-
PHOSPHOCHOLINE + A FATTY ACID ANION.
CC -1- SUBUNIT: DIMER OF DISSIMILAR CHAINS LINKED BY ONE OR MORE
DISULFIDE BONDS. THE A CHAINS HAVE PHOSPHOLIPASE A2 ACTIVITY AND
THE B CHAINS SHOW HOMOLOGU WITH THE BASIC PROTEASE INHIBITORS.
CC -1- MISCELLANEOUS: THE A3 CHAIN IS FOUND IN BETA-5 BUNGAROTOXIN.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
DR PIR: A00758; PSKFAU.
DR HSSP: P15445; 1A3F.
DR InterPro: IPR001211; .
DR Pfam: PF00068; phoslip; 1.
DR PRINTS: PR00389; PHPLIPASEA2.
DR PROSITE: PS00118; PA2_HIS; 1.
DR PROSITE: PS00119; PA2_ASP; 1.
KW Hydrolyase; Lipid degradation; Calcium; Multigene family; Venom;
KM Presynaptic neurotoxin.
FT ACT_SITE 48 48 BY SIMILARITY.
FT ACT_SITE 94 94 BY SIMILARITY.
FT DISULFID 15 15 INTERCHAIN (WITH A B CHAIN) (PROBABLE).
FT DISULFID 27 119 BY SIMILARITY.
FT DISULFID 29 45 BY SIMILARITY.
FT DISULFID 44 100 BY SIMILARITY.
FT DISULFID 51 93 BY SIMILARITY.
FT DISULFID 61 86 BY SIMILARITY.
FT DISULFID 79 91 BY SIMILARITY.
FT CA_BIND 49 49 BY SIMILARITY.
SQ SEQUENCE 120 AA; 13439 MW; 0301BF045AB31770 CRC64;

Query Match 62.1%; Score 36; DB 1; Length 120;
Best Local Similarity 83.3%; Pred. No. 27;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KTWGOY 6
ID PA22_BUNMU STANDARD; PRT; 145 AA.
AC P00618;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PHOSPHOLIPASE A2, BETA BUNGAROTOXIN A2 CHAIN PRECURSOR (EC 3.1.1.4)
(PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE).
OS Bungarus multicinctus (Many-banded Krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylidae; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Bungarinae; Bungarus.
OX NCBI_TaxID=8616;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Venom gland;
RX MEDLINE-90356416; PubMed-2388842;
RA Danse J.M., Toussaint J.L., Kempf J.;
RT "Nucleotide sequence encoding beta-bungarotoxin A2-chain from the
venom glands of Bungarus multicinctus.";
RL Nucleic Acids Res. 18:4609-4609(1990).
RN [2]

RP SEQUENCE OF 26-145.
RC TISSUE-Venom;
RA MEDLINE-82239270; PubMed-7096305;
RX Kondou K., Toda H., Narita K., Lee C.-Y.;
RT "Amino acid sequences of three beta-bungarotoxins (beta 3-, beta 4-,
RT and beta 5-bungarotoxins) from Bungarus multicinctus venom. Amino
RT acid substitutions in the A chains.";
RL J. Biochem. 91:1531-1548(1982)
CC -1- FUNCTION: INHIBITS NEUROMUSCULAR TRANSMISSION BY BLOCKING
CC ACETYLCHOLINE RELEASE FROM THE NERVE TERMINI. ACT PRESYNAPTICALLY.
CC -1- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE
CC 2-ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES.
CC -1- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O - 1-ACYLGLYCERYL-
CC PHOSPHOCHOLINE + A FATTY ACID ANION.
CC -1- SUBUNIT: DIMER OF DISSIMILAR CHAINS LINKED BY ONE OR MORE
CC DISULFIDE BONDS. THE A CHAINS HAVE PHOSPHOLIPASE A2 ACTIVITY AND
CC THE B CHAINS SHOW HOMOLOGU WITH THE BASIC PROTEASE INHIBITORS. THE
CC A2 CHAIN IS FOUND IN BETA-3 AND BETA-4 BUNGAROTOXINS.
CC -1- MISCELLANEOUS: LD(50) IS 0.066 MG/KG BY INTRAPERITONEAL INJECTION
CC IN BETA-3 BUNGAROTOXIN AND 0.073 MG/KG BY INTRAPERITONEAL INJECTION
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
CC -----
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CC -----
DR EMBL: X53407; CAA37483.1; -
DR PIR: S10980; PSKFA2.
DR HSSP: P15445; 1A3P.
DR InterPro: IPR001211; -
DR Pfam: PF00068; Phoslip; 1.
DR PRINTS: PR00389; PHPLIPASEA2.
DR PROSITE: PS00118; PA2_HIS; 1.
DR PROSITE: PS00119; PA2_ASP; 1.
DR Hydroxylase: Lipid degradation; Calcium; Multigene family; Venom;
KW Presynaptic neurotoxin; Signal.
FT SIGNAL 1 25
FT CHAIN 26 145
FT FT
FT ACT_SITE 73 73 PHOSPHOLIPASE A2, BETA BUNGAROTOXIN A2
FT ACT_SITE 119 119 CHAIN.
FT DISULFID 40 40 BY SIMILARITY.
FT DISULFID 52 144 INTERCHAIN (WITH A B CHAIN) (PROBABLE).
FT DISULFID 54 70 BY SIMILARITY.
FT DISULFID 69 125 BY SIMILARITY.
FT DISULFID 76 118 BY SIMILARITY.
FT DISULFID 86 111 BY SIMILARITY.
FT DISULFID 104 116 BY SIMILARITY.
FT CA_BIND 74 74 BY SIMILARITY.
FT CA_BIND 91 92 QS -> SQ (IN REF. 2).
FT CONFLICT 128 128 N -> Q (IN REF. 2).
FT CONFLICT 130 130 E -> D (IN REF. 2).
SQ SEQUENCE 145 AA; 16296 MW; 08CD9D0E84E5781 CRC64;

Query Match 62.1%; Score 36; DB 1; Length 145;
Best Local Similarity 83.3%; Pred. No. 32;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KTWGOY 6
|11111|
Db 42 KTWGEY 47

RESULT 30
PA24_BUNMU STANDARD; PRT; 147 AA.
ID PA24_BUNMU
AC: P17934;
DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE PHOSPHOLIPASE A2, BETA BUNGAROTOXIN A4 CHAIN PRECURSOR (EC 3.1.1.4)
DE (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE).
OS Bungarus multicinctus (Many-banded krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Bungarinae; Bungarus.
OX NCBI_TaxID=8616;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Venom gland;
RX MEDLINE-90356417; PubMed-2388843;
RA Danse J.M., Garnier J.M., Kempf J.;
RT "CDNA deduced amino-acid sequence of a new phospholipase from
RT Bungarus multicinctus.";
RL Nucleic Acids Res. 18:4610-4610(1990).
CC -1- FUNCTION: INHIBITS NEUROMUSCULAR TRANSMISSION BY BLOCKING
CC ACETYLCHOLINE RELEASE FROM THE NERVE TERMINI. ACT PRESYNAPTICALLY.
CC -1- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE
CC 2-ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES.
CC -1- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O - 1-ACYLGLYCERYL-
CC PHOSPHOCHOLINE + A FATTY ACID ANION.
CC -1- SUBUNIT: DIMER OF DISSIMILAR CHAINS LINKED BY ONE OR MORE
CC DISULFIDE BONDS. THE A CHAINS HAVE PHOSPHOLIPASE A2 ACTIVITY AND
CC THE B CHAINS SHOW HOMOLOGU WITH THE BASIC PROTEASE INHIBITORS.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X53408; CAA37484.1; -
DR PIR: S10982; PSKFA4.
DR HSSP: P15445; 1A3P.
DR InterPro: IPR001211; -
DR Pfam: PF00068; Phoslip; 1.
DR PRINTS: PR00389; PHPLIPASEA2.
DR PROSITE: PS00118; PA2_HIS; 1.
DR PROSITE: PS00119; PA2_ASP; 1.
DR Hydroxylase: Lipid degradation; Calcium; Multigene family; Venom;
KW Presynaptic neurotoxin; Signal.
FT SIGNAL 1 27
FT CHAIN 28 147
FT FT
FT ACT_SITE 75 75 PHOSPHOLIPASE A2, BETA BUNGAROTOXIN A4
FT ACT_SITE 119 119 CHAIN.
FT DISULFID 42 42 BY SIMILARITY.
FT DISULFID 54 146 INTERCHAIN (WITH A B CHAIN) (PROBABLE).
FT DISULFID 56 72 BY SIMILARITY.
FT DISULFID 71 127 BY SIMILARITY.
FT DISULFID 78 120 BY SIMILARITY.
FT DISULFID 88 113 BY SIMILARITY.
FT DISULFID 106 118 BY SIMILARITY.
FT CA_BIND 76 76 BY SIMILARITY.
SQ SEQUENCE 147 AA; 16177 MW; 20CC4BF63F8CE2B6 CRC64;

Query Match 62.1%; Score 36; DB 1; Length 147;
Best Local Similarity 83.3%; Pred. No. 33;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KTWGOY 6
|11111|
Db 44 KTWGEY 49

Search completed: July 3, 2001, 10:28:37

Job time: 322 sec

7

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2001, 10:00:55 ; Search time 33.34 Seconds
(without alignments)
16.365 Million cell updates/sec

Title: US-09-214-836-1

Perfect score: 58

Sequence: 1 KTWGQYNAV 9.

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext: 0.5

Searched: 412676 seqs, 60623988 residues

412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq_0601:*

- 1: /SIDSR/gcgdata/geneseq/AA1980.DAT:*
- 2: /SIDSR/gcgdata/geneseq/AA1981.DAT:*
- 3: /SIDSR/gcgdata/geneseq/AA1982.DAT:*
- 4: /SIDSR/gcgdata/geneseq/AA1983.DAT:*
- 5: /SIDSR/gcgdata/geneseq/AA1984.DAT:*
- 6: /SIDSR/gcgdata/geneseq/AA1985.DAT:*
- 7: /SIDSR/gcgdata/geneseq/AA1986.DAT:*
- 8: /SIDSR/gcgdata/geneseq/AA1987.DAT:*
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- 10: /SIDSR/gcgdata/geneseq/AA1989.DAT:*
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- 14: /SIDSR/gcgdata/geneseq/AA1993.DAT:*
- 15: /SIDSR/gcgdata/geneseq/AA1994.DAT:*
- 16: /SIDSR/gcgdata/geneseq/AA1995.DAT:*
- 17: /SIDSR/gcgdata/geneseq/AA1996.DAT:*
- 18: /SIDSR/gcgdata/geneseq/AA1997.DAT:*
- 19: /SIDSR/gcgdata/geneseq/AA1998.DAT:*
- 20: /SIDSR/gcgdata/geneseq/AA1999.DAT:*
- 21: /SIDSR/gcgdata/geneseq/AA2000.DAT:*
- 22: /SIDSR/gcgdata/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	9	19	AAW45771
2	53	91.4	9	16	AAW78644
3	53	91.4	9	19	AAW77119
4	53	91.4	9	19	AAW78850
5	53	91.4	9	19	AAW70010
6	53	91.4	9	19	AAW54598
7	53	91.4	9	19	AAW45777
8	53	91.4	9	19	AAW45770
9	53	91.4	9	20	AAW49663
10	53	91.4	9	20	AAW58524
11	53	91.4	9	20	AAW47616

12	53	91.4	9	20	AAW33172	Human gp100-Pmel11
13	53	91.4	9	20	AAW40211	Amino acid sequenc
14	53	91.4	9	20	AAW28667	Melanoma-derived I
15	53	91.4	9	20	AAW01753	Exemplary antigen
16	53	91.4	9	20	AAW00715	Tumour antigen bo
17	53	91.4	9	20	AAW10449	HLA Class I motif
18	53	91.4	9	21	AAW33662	MHC class I associ
19	53	91.4	9	21	AAW23679	Cytotoxic T lympha
20	53	91.4	9	21	AAW08694	Antigenic peptide
21	53	91.4	9	21	AAW71520	Human gp100 Pmel11
22	53	91.4	9	21	AAW02622	Tumour associated
23	53	91.4	9	21	AAW90803	Human leukocyte an
24	53	91.4	9	21	AAW92299	gp100-Pmel117 anti
25	53	91.4	9	21	AAW84296	Tumour associated
26	53	91.4	9	21	AAW82879	gp100-Pmel117) tum
27	53	91.4	9	21	AAW56614	gp100-Pmel-117 gen
28	53	91.4	9	22	AAW31354	Exemplary antigen
29	53	91.4	10	16	AAW78643	Immunogenic peptid
30	53	91.4	10	16	AAW84209	gp100 melanoma ant
31	53	91.4	11	16	AAW78642	Immunogenic peptid
32	53	91.4	30	22	AAW61647	gp100 peptide #1.
33	53	91.4	661	16	AAW84855	MART-1 melanoma an
34	53	91.4	661	16	AAW78646	Melanoma associate
35	53	91.4	661	20	AAW31977	Human melanoma ant
36	53	91.4	662	20	AAW42627	Human melanoma ant
37	53	91.4	668	18	AAW38164	Pmel17 encoded by
38	52	89.7	9	19	AAW45775	Melanoma associate
39	52	89.7	9	19	AAW45776	Melanoma associate
40	50	86.2	9	19	AAW42542	Gp 100 epitope (re
41	50	86.2	9	20	AAW46537	Immunogenic peptid
42	50	86.2	9	21	AAW13727	Peptide fragment #
43	50	86.2	10	16	AAW84208	gp100 melanoma ant
44	50	86.2	661	16	AAW84854	MART-1 melanoma an
45	49	84.5	625	20	AAW31978	Mouse melanoma ant

ALIGNMENTS

RESULT 1	
AAW45771	standard; peptide; 9 AA.
XX	
AC	AAW45771;
XX	
DT	22-JUN-1998 (first entry)
XX	
DE	Melanoma associated peptide analogue #2.
XX	
KW	Metastatic melanoma; peptide analogue; vaccine; cancer; diagnosis;
XX	antigen; CTL; immunogenic; viral disease.
OS	Synthetic.
OS	Homo sapiens.
PN	WC09802538-A1.
XX	
PD	22-JAN-1998.
XX	
PF	08-JUL-1997; 97WO-EP03712.
XX	
PR	11-JUL-1996; 96EP-0201945.
XX	
PA	(ALKU) AKZO NOBEL NV.
XX	
PI	Adema GJ, Figdor CG;
XX	
DR	WPI; 1998-110586/10.
XX	
PT	Melanoma associated peptide analogues - useful in vaccines against
PT	melanoma
XX	
PS	Claim 4; Figure 1; 47pp; English.

```

XX This sequence represents a specifically claimed example of a novel
CC peptide, which is immunogenic with lymphocytes directed against
CC metastatic melanomas. It is characterized in that it comprises at least
CC a part of the following sequence, where the amino acid at position 2 or 8
CC is substituted: Lys-Thr-Tyr-Gln-Tyr-Tyr-Gln-Val. Vaccines comprising
CC the peptide, an epitope of the peptide, nucleotide sequence encoding the
CC peptide, or an antigen presenting cell preloaded with the peptide or
CC antibody as above, are useful for cancer, particularly melanoma,
CC treatment. The peptides can also be used to generate antigen reactive
CC tumour infiltrating lymphocytes, which can also be used in vaccines. The
CC peptides can be exploited to elicit native epitope-reactive CTL. Usage
CC of the peptides with improved immunogenicity may contribute to the
CC development of CTL-epitope based vaccines in viral disease and cancer.
CC
XX Sequence 9 AA;
SQ

```

Query Match 100.0%; Score 58; DB 19; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 KTWGQYNAV 9
   |||||
DB 1 ktwgqywav 9

```

RESULT 2
 AAR78644
 ID AAR78644 standard; Protein; 9 AA.
 AC AAR78644;
 XX
 DT 22-JAN-1996 (first entry)
 XX
 DE Immunogenic peptide of melanoma associated antigen gp100.
 XX
 KM Melanoma; antigen; vaccine; immunogen; primer; probe; detection;
 KW Identification; tumour; gp100.
 XX
 OS Homo sapiens.
 XX
 PN EP668350-A1.
 XX
 PD 23-AUG-1995.
 XX
 PF 14-FEB-1995; 95EP-0200348.
 XX
 PR 21-DEC-1994; 94EP-0203709.
 PR 16-FEB-1994; 94EP-0200337.
 XX
 PA (ALKU) AKZO NOBEL NV.
 XX
 PI Adema GJ, Figdor CG;
 XX
 DR WPI; 1995-284790/38.
 DR N-PSDB; AA096055.
 XX
 PT Melanoma associated antigen gp100 - used in vaccines and for the
 PT detection of tumours
 XX
 PS Claim 5; Page 31; 40pp; English.
 XX
 CC Immunogenic peptides derived from the melanoma associated antigen
 CC (See AAR78639-45) may be used in the production of vaccines.
 CC Nucleotide sequences encoding the immunogenic peptides may be used
 CC as primers and probes in the detection of melanoma cells. Tumour
 CC infiltrating lymphocytes capable of binding to the melanoma
 CC associated antigen can be cultured ex vivo and returned to melanoma
 CC particles, and when radiolabelled, they may be used to identify
 CC tumour deposits.
 CC
 XX Sequence 9 AA;
 SQ

```

OY 1 KTWGQYNAV 9
   |||||
DB 1 ktwgqywav 9

```

Query Match 91.4%; Score 53; DB 16; Length 9;
 Best Local Similarity 88.9%; Pred. No. 3.4e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 3
 AAW77119
 ID AAW77119 standard; peptide; 9 AA.
 AC AAW77119;
 XX
 DT 16-NOV-1998 (first entry)
 XX
 DE gp100/Pmel17 synthetic peptide epitope 1.
 XX
 KW Tyrosinase; tyrosinase cytotoxic lymphocyte response;
 KW cytotoxic T lymphocyte; cysteine-depleted; melanoma.
 XX
 OS Synthetic.
 XX
 PN WO9833810-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 29-JAN-1998; 98WO-US01592.
 XX
 PR 30-JAN-1997; 97US-0037781.
 XX
 PA (UYVI-) UNIV VIRGINIA PATENT FOUND.
 XX
 PI Engelhard VH, Hunt DF, Kittlesen D, Slingluff CL;
 XX
 DR WPI; 1998-437388/37.
 XX
 PT Disease specific immunogen - comprises disease specific cytotoxic T
 PT lymphocyte epitope used to elicit melanoma specific CTL response
 XX
 PS Disclosure; Page 27; 93pp; English.
 XX
 CC The peptide epitope AAW77119-W77138 were created for human
 CC tumour-specific cytotoxic T lymphocyte response. These peptides are
 CC cysteine-depleted mutants of a native disease-specific CTL epitope. The
 CC response than the native epitope. The epitopes can be used in a
 CC disease-specific immunogen to protect a mammal against disease in
 CC particular melanomas. The peptides may also be used to screen a sample
 CC for the presence of an antigen with the same epitope, or with a different
 CC cross-reactive epitope.
 CC
 XX Sequence 9 AA;
 SQ

Query Match 91.4%; Score 53; DB 19; Length 9;
 Best Local Similarity 88.9%; Pred. No. 3.4e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

OY 1 KTWGQYNAV 9
   |||||
DB 1 ktwgqywav 9

```

RESULT 4
 AAW78850
 ID AAW78850 standard; peptide; 9 AA.
 AC AAW78850;
 XX
 XX

DT	17-NOV-1998	(first entry)
DE	PMEL 17 (GP100) protein fragment 154-162.	
XX		
XX		
KM	Microparticle; delivery; polymeric matrix; autoantigen; tumour antigen;	
KW	class II associated peptide; pathogen; gene therapy; genetic disease;	
XX	infection; downregulation; immune response.	
OS	Homo sapiens.	
OS	Synthetic.	
PN	WO9831398-A1.	
XX		
PD	23-JUL-1998.	
XX		
PF	22-JAN-1998; 98WO-US01499.	
XX		
PR	06-JAN-1998; 98US-0003253.	
PR	22-JAN-1997; 97US-0787547.	
PA	(PANG-) PANGAEA PHARM INC.	
XX		
PT	Curley JM, Hedley ML, Langer RS, Lunsford LB;	
DR	WPI; 1998-427556/36.	
XX		
PT	New preparations of microparticles - comprising a synthetic polymer	
PT	matrix and nucleic acid comprising an expression vector for use in	
XX	gene therapy	
PS	Disclosure; Page 10; 101pp; English.	
XX		
CC	A microparticle preparation (MP) has been developed, consisting of	
CC	microparticles having a diameter of less than 100 nm. The MP	
CC	comprises: (a) a polymeric matrix (PM) consisting of one or more	
CC	synthetic polymers having a solubility in water of less than 1 mg/l; and	
CC	(b) an expression vector selected from RNA molecules (at least 50% of	
CC	which are closed circles) or circular plasmid DNA (at least 50% of which	
CC	are supercoiled). Also described is a MP of at most 20 microns in	
CC	diameter, comprising: (a) a PM; and (b) a NM comprising an expression	
CC	control sequence operatively linked to a coding sequence, where the	
CC	coding sequence encodes an expression product selected from: (1) a	
CC	polypeptide at least 7 amino acids in length, having a sequence identical	
CC	to the sequence of: (1) a fragment of a naturally-occurring mammalian	
CC	protein; or (11) a fragment of a naturally-occurring protein from an	
CC	infectious agent which infects a mammal; (2) a peptide having a length	
CC	and sequence which permits it to bind to an MHC class I or II molecule;	
CC	and (3) the polypeptide or the peptide linked to a trafficking sequence.	
CC	AAW69763 to AAW69765, and AAW78793 to AAW78897 are peptide fragments for	
CC	use in the present invention. The MPs are highly effective vehicles for	
CC	the delivery of polynucleotides into phagocytic cells. They can be used	
CC	for gene therapy, e.g. for treating genetic diseases, infections or	
CC	tumours or for downregulating an immune response.	
XX		
XX		
Sequence	9 AA:	
XX		
Query Match	91.4%; Score 53; DB 19; Length 9;	
Best Local Similarity	88.9%; Pred. No. 3.4e+05;	
Matches	8; Conservative 0; Mismatches 1; Indels 0; Gaps 0	
OY	1 KTWGQYWAY 9	
DB	1	
	1 KTWGQYWAY 9	
RESULT	5	
AAW70010		
ID	AAW70010 standard; peptide; 9 AA.	
AC		
AAW70010;		
XX		
22-OCT-1998	(first entry)	

```

DE XX Melanoma-associated antigen gp100 derived HLA-A2.1 binding peptide 1.
KW KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KV human leukocyte antigen; HLA; tumor associated antigen; cancer;
KW antigen presenting cell; APC; immunogenic peptide; immune disorder;
KW viral infection; AIDS; hepatitis; bacterial infection; malaria;
KW fungal infection; tuberculosis; melanoma; gp100.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN MO9833888-A1.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01959.
XX
PR 31-JAN-1997; 97US-0036966.
XX
PP (EPIM-) EPIMADNE INC.
PA
PI Cells E, Sette A, Sidney J, Southwood S, Tsai V;
XX
DR WPI: 1998-437445/37.
XX
XX Production of antigen-specific cytotoxic T cells - by incubating
PT immunogenic peptide(s) from antigen that binds class I major
PT histocompatibility complex molecules with pre-created antigen
PT presenting cells
XX
PS Example 4; Page 62; 104pp; English.
XX
CC Sequences shown in AAW70010 to AAW70026 represent peptides derived from
CC melanoma-associated antigen gp100 that can bind to a human leukocyte
CC antigen (HLA), HLA-A2.1. The peptides are used to exemplify the method
CC of invention of producing antigen-specific cytotoxic T cells (CTLs) in
CC vitro. The method comprises contacting immunogenic peptides from an
CC antigen that binds class I major histocompatibility complex (MHC)
CC molecules with antigen presenting cells (APCs) pretreated with
CC pretreatment growth factors, and incubating the APCs with purified CD8
CC cells in the presence of at least 2 incubation growth factors, thereby
CC producing antigen-specific CTLs. A method for specifically killing
CC target cells in a human patient is also provided which comprises
CC obtaining a fluid sample containing CTLs from a patient, contacting the
CC cytotoxic T cells with APCs pretreated with pre-treatment growth
CC factors, where the APCs comprise class I MHC molecules. The pretreated
CC APCs are incubated with the cytotoxic growth factors, thereby producing
CC activated CTLs which are contacted with a carrier to form a composition.
CC The composition can then be administered to the patient. The activated
CC CTLs can be used for treating cancers, immune disorders, viral
CC infections, AIDS, hepatitis, bacterial infection, fungal infection,
CC malaria or tuberculosis.
CC
SQ Sequence 9 AA:
OY Query Match 91.4%; Score 53; DB 19; Length 9;
ID Best Local Similarity 88.9%; Pred. No. 3.4e+05;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB 1 KTWGQYWAY 9
1 ktwgqyway 9
RESULT 6
AAWS4598
ID AAWS4598 standard; peptide: 9 AA.
XX
XX AAWS4598;
XX
DT 25-SEP-1998 (first entry)

```

XX Peptide 3 from gp 100/Pmel-17.
DE
XX Mannose; antigen; antigen-presenting cell; mannosylated peptide; T cell;
KM vaccine; treatment.
XX
XX Synthetic.
OS
XX WO9813378-A1.
PN
XX
PD 02-APR-1998.
XX
XX 25-SEP-1997; 97WO-NL00536.
PF
XX 26-SEP-1996; 96EP-0202701.
PR
XX (UYLE-) RIJKSUNIV LEIDEN.
PA
XX DrJfhout JW, Konling F;
XX
XX WPI; 1998-230631/20.
DR
XX
XX Increasing uptake and presentation of antigen(s) - by adding mannose
PT residue(s) to antigen for increasing T cell response, useful in,
PT e.g. vaccines against viral infection(s)
PS
XX Disclosure; Page 24; 47pp; English.
PS
XX The peptides AAW54559-W54809 are examples of peptides to which at least
CC 1 (preferably 2) mannose can be attached to increase their uptake as
CC antigens by antigen-presenting cells. Uptake of agonist mannosylated
CC peptides will increase the T cell response, whereas uptake of antagonist
CC peptides blocks the T cell response. Blocking binding of immunogenic
CC autoantigens can be used in treatment of type I diabetes, rheumatoid
CC arthritis, graft rejection etc., also to induce T-cell non-
CC responsiveness. Vaccines containing mannosylated antigen are used to
CC prevent or treat infections by, e.g. bacteria, viruses, fungi, helminths
CC and parasites.
CC
SQ Sequence 9 AA;

Query Match 91.4%; Score 53; DB 19; Length 9;
Best Local Similarity 88.9%; Pred. No. 3.4e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYWAY 9
DB 1 ktwgqyway 9

RESULT 7
AAW5777
ID AAW5777 standard; peptide; 9 AA.
XX
AC AAW5777;
XX
XX 22-JUN-1998 (first entry)
DT
XX
XX Melanoma associated peptide analogue #8.
DE
XX
XX Metastatic melanoma; peptide analogue; vaccine; cancer; diagnosis;
KM antigen; CTL; immunogenic; viral disease.
KW
XX
XX Synthetic.
OS
XX Homo sapiens.
OS
XX WO9802538-A1.
PN
XX
XX 22-JAN-1998.
PD
XX
PF 08-JUL-1997; 97WO-EP03712.
XX

PR 11-JUL-1996; 96EP-0201945.
XX
XX (ALKU) AKZO NOBEL NV.
PA
XX
XX Adema GJ, Figdor CG;
PI
XX
XX WPI; 1998-110586/10.
DR
XX
XX
PT Melanoma associated peptide analogues - useful in vaccines against
PT melanoma
XX
XX
PS Claim 4; Page 35; 47pp; English.
PS
XX This sequence represents a specifically claimed example of a novel
CC peptide, which is immunogenic with lymphocytes directed against
CC metastatic melanomas. It is characterised in that it comprises at least
CC a part of the following sequence, where the amino acid at position 2 or 8
CC is substituted: Lys-Thr-Tip-Gln-Tyr-Tip-Gln-Val. Vaccines comprising
CC the peptide, an epitope of the peptide, nucleotide sequence encoding the
CC peptide, or an antigen presenting cell preloaded with the peptide or
CC antibody as above, are useful for cancer, particularly melanoma,
CC treatment. The peptides can also be used to generate antigen reactive
CC tumour infiltrating lymphocytes, which can also be used in vaccines. The
CC peptides can be exploited to elicit native epitope-reactive CTL. Usage
CC of the peptides with improved immunogenicity may contribute to the
CC development of CTL-epitope based vaccines in viral disease and cancer.
XX
SQ Sequence 9 AA;

Query Match 91.4%; Score 53; DB 19; Length 9;
Best Local Similarity 88.9%; Pred. No. 3.4e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYWAY 9
DB 1 ktwgqyway 9

RESULT 8
AAW5770
ID AAW5770 standard; peptide; 9 AA.
XX
AC AAW5770;
XX
XX 22-JUN-1998 (first entry)
DT
XX
XX Melanoma associated peptide analogue #1.
DE
XX
XX Metastatic melanoma; peptide analogue; vaccine; cancer; diagnosis;
KM antigen; CTL; immunogenic; viral disease.
KW
XX
XX Synthetic.
OS
XX Homo sapiens.
OS
XX WO9802538-A1.
PN
XX
XX 22-JAN-1998.
PD
XX
XX 08-JUL-1997; 97WO-EP03712.
PF
XX
XX 11-JUL-1996; 96EP-0201945.
PR
XX
XX (ALKU) AKZO NOBEL NV.
PA
XX
XX Adema GJ, Figdor CG;
PI
XX
XX WPI; 1998-110586/10.
DR
XX
XX Melanoma associated peptide analogues - useful in vaccines against
PT melanoma
PT
XX
PS Claim 1; Figure 1; 47pp; English.

XX This sequence represents a specifically claimed example of a novel
CC peptide, which is immunogenic with lymphocytes directed against
CC metastatic melanomas. It is characterised in that it comprises at least
CC a part of the following sequence, where the amino acid at position 2 or 8
CC is substituted: Lys-Thr-Trp-Gln-Tyr-Gln-Val. Vaccines comprising
CC the peptide, an epitope of the peptide, nucleotide sequence encoding the
CC peptide, or an antigen presenting cell preloaded with the peptide or
CC antibody as above, are useful for cancer, particularly melanoma,
CC treatment. The peptides can also be used to generate antigen reactive
CC tumour infiltrating lymphocytes, which can also be used in vaccines. The
CC peptides can be exploited to elicit native epitope-reactive CTL. Usage
CC of the peptides with improved immunogenicity may contribute to the
CC development of CTL-epitope based vaccines in viral disease and cancer.
XX

SQ Sequence 9 AA:

Query Match 91.4%; Score 53; DB 19; Length 9;
Best Local Similarity 88.9%; Pred. No. 3.4e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTMGQYMAV 9
Db 1 ktwgqywmv 9
|||||||
1

RESULT 9
AAV49663
ID AAV49663 standard; peptide; 9 AA.
XX
AC AAV49663:
XX
DT 14-JAN-2000 (first entry)
XX
DE Tumour antigenic peptide SEQ ID NO:30.
XX
KW Human; sdph3.10; SAGE; sdg3.8; HAGE; sdd3.5; TRAP; sarcoma;
KM tumour rejection antigen precursor; tumour associated nucleic acid;
KW carcinoma; cancer; immune response; diagnosis.
XX
OS Synthetic.
XX
PN WO9953061-A2.
XX
PD 21-OCT-1999.
XX
PF 14-APR-1999; 99WO-US08163.
XX
PR 15-APR-1998; 98US-0060706.
PR 27-JUL-1998; 98US-0122989.
PR 30-OCT-1998; 98US-0183706.
PR 30-OCT-1998; 98US-0183789.
XX
PA (LUDWIG) INST CANCER RES.
XX
PI Martelange V, De Smet C, Boon-Falleur T;
XX
DR WPI; 1999-620430/53.
XX
PT New nucleic acid encoding sarcoma-associated gene products, useful for
PT diagnosing, e.g. treating and preventing cancer -
XX
PS Disclosure; Page 25; 93pp; English.

XX The present invention describes sarcoma-associated gene products (I).
CC Agents, specifically sarcoma associated nucleic acids (II) or their
CC expression products that are tumour rejection antigens (TRA), that
CC selectively increase formation of HLA (human leucocyte antigen)/(I)
CC complexes are used for treating cancer, especially sarcoma and
CC carcinoma, in humans and other animals. Compositions containing
CC autologous cytolytic T cells (CTL), specific for the HLA/(I) complex,
CC are similarly useful, also transformed cells that stimulate such CTL

CC in vivo. (II) are also used: (i) as source of therapeutic antisense
CC sequences that reduce expression of (II); (ii) for recombinant
CC production of (I); (iii) particularly its fragments, as primers and
CC probes in usual hybridisation and amplification assays, for diagnosis,
CC prognosis and monitoring of tumours, or for measuring binding
CC specificity of HLA molecules or CTL clones; (iv) to identify related
CC sequences; and (v) for generating transgenic animals, e.g. for studying
CC cancer and immune responses to it. (I) are used to raise specific
CC antibodies (Ab) and therapeutically. Ab are used to diagnose tumours in
CC immunoassays, also for delivering drugs, toxins, imaging agents etc. to
CC (I)-expressing cells. AAV49637 to AAV49670 represent exemplary tumour
CC antigenic peptides given in the present invention.
XX

SQ Sequence 9 AA:

Query Match 91.4%; Score 53; DB 20; Length 9;
Best Local Similarity 88.9%; Pred. No. 3.4e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTMGQYMAV 9
Db 1 ktwgqywmv 9
|||||||
1

RESULT 10
AAV53524
ID AAV53524 standard; Protein; 9 AA.
XX
AC AAV53524:
XX
DT 18-JAN-2000 (first entry)
XX
DE Human melanoma Pmel17 (gp100) (aa 154-162) binds HLA-A2.
XX
KW Lipopeptide; epitope; cytotoxic T lymphocyte; CTL; lipid; spacer; p53;
KM electrical charge; hydrophilicity; Vaccine; immune response; HIV; HBV;
KW human immunodeficiency virus; hepatitis B virus; papilloma virus;
KW melanoma; malaria; parasite.
XX
OS Synthetic.
XX
PN FR2776926-A1.
XX
PD 08-OCT-1999.
XX
PF 07-APR-1998; 98FR-0004323.
XX
PR 07-APR-1998; 98FR-0004323.
XX
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (INSP) INST PASTEUR LILLE.
XX
PI Le Gal FA, Guillet JG, Gahery SH, Gras MH, Melnyk O, Tartar A;
XX
DR WPI; 1999-583113/50.
XX
PT New lipopeptide containing lipid regions and two epitopes, all
PT separated by peptide spacers that impart hydrophilicity, useful in
PT vaccines -
XX
PS Disclosure; Page 24; 35pp; French.

XX The invention relates to the generation of a lipopeptide comprising at
CC least one auxiliary T epitope, at least one cytotoxic T lymphocyte (CTL)
CC epitope and at least one lipid residue with (i) the epitopes and lipid
CC portion and (ii) the epitopes, being separated independently by peptide
CC spacers. These spacers comprise sequences of amino acids which carry an
CC overall electrical charge in neutral media to ensure that the
CC lipopeptide is hydrophilic. The peptides AAV53301-Y53549 represents
CC examples of peptide epitopes used to generate the lipopeptides. These are

CC used in therapeutic or prophylactic compositions and vaccines to induce
CC specific immune responses against human immunodeficiency, hepatitis B or
CC papilloma viruses; p53 of melanoma or the malaria parasite.
XX
SQ Sequence 9 AA;

Query Match 91.4%; Score 53; DB 20; Length 9;
Best Local Similarity 88.9%; Pred. No. 3.4e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KTWGQYMAV 9
111111111
Db 1 KTWGQYMAV 9

RESULT 11
AAV47616
ID AAV47616 standard; peptide; 9 AA.
XX
AC AAV47616;
XX
DT 01-DEC-1999 (first entry)
XX
DE Immunogenic peptide having a human leukocyte antigen binding motif #2227.
XX
KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
KW immune response; T cell activation; major histocompatibility complex;
KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
KW vaccine; immunisation.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO945954-A1.
XX
PD 16-SEP-1999.
XX
PF 13-MAR-1998; 98WO-US05039.
XX
PR 13-MAR-1998; 98WO-US05039.
XX
PA (EPRM-) EPRIMUNE INC.
XX
PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
XX
DR WPI: 1999-551214/46.
XX
PT New immunogenic peptides with HLA binding motif, useful in treatment
XX and diagnosis of cancers and viral diseases
XX
PS Claim 1; Page 116; 150pp; English.
XX
CC AAV45390 to AAV48214 represent specifically claimed immunogenic peptides
CC having a human major histocompatibility complex (MHC) Class I (also
CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic
CC peptides can bind to a specific HLA allele (i.e., HLA-A subtypes
CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
CC response against the antigen from which the peptide is derived.
CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
CC normally induced by an antigen in the form of a peptide fragment bound
CC to a HLA molecule, rather than the intact foreign antigen itself, and
CC are particularly important in tumour rejection and in fighting viral
CC infections. The peptides are therefore useful therapeutically to treat
CC or prevent viral infections and cancers in mammals (especially humans)
CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
CC They can be administered as vaccines to elicit an immune response in
CC individuals susceptible or otherwise at risk of viral infection or
CC cancer, or used to treat chronic or acute conditions. They are also
CC useful diagnostically, and can be used to induce a cytotoxic T cell
CC response, by contacting a cytotoxic T cell with the peptide e.g. to
CC produce CTLs ex vivo for infusion back into a patient. The

CC polynucleotides encoding the immunogenic peptides are also useful
CC therapeutically and for immunisation as above.
XX
SQ Sequence 9 AA;

Query Match 91.4%; Score 53; DB 20; Length 9;
Best Local Similarity 88.9%; Pred. No. 3.4e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KTWGQYMAV 9
111111111
Db 1 KTWGQYMAV 9

RESULT 12
AAV33172
ID AAV33172 standard; peptide; 9 AA.
XX
AC AAV33172;
XX
DT 17-NOV-1999 (first entry)
XX
DE Human gp100-Pmel17 peptide #1.
XX
KW Human; protein delivery; Yersinia sp.; effector gene; mutant; antigen;
KW immune response; cytotoxic T-lymphocyte; CTL; vaccination; treatment;
KW pathological disorder; gp100-Pmel17.
XX
OS Homo sapiens.
XX
PN WO945098-A2.
XX
PD 10-SEP-1999.
XX
PF 03-MAR-1999; 99WO-IB00587.
XX
PR 06-MAR-1998; 98US-0036582.
XX
PA (VBRU/) VAN DER BRUGGEN P B.
PA (CORNU/) CORNELIS G R.
PA (BOLA/) BOLAND A M.
PA (BOON/) BOON-FALLEUR T R.
XX
PI Van Der Bruggen PB, Cornelis GR, Boland AM, Boon-Falleur TR;
XX
DR WPI: 1999-540840/45.
XX
PT New mutant Yersinia strains useful for treating a pathological disorder
XX
PS Example 1; Page 71; 80pp; English.
XX
CC This invention describes a novel mutant Yersinia (Y1) strain, comprising
CC mutation(s) in effector-encoding gene(s) and deficient in the production
CC of functional effector protein(s). The invention describes (1) a
CC quintuple mutant Yersinia strain, having the designation Yersinia
CC enterocolitica YOPBOMP or Yersinia pseudotuberculosis YOPBHAOU; (2) an
CC expression vector (EV1) for delivering a heterologous protein into a
CC eukaryotic cell, comprising in the 5'-3' direction: (3) a Yersinia or
CC mutant Yersinia strain for delivering a heterologous protein into a
CC eukaryotic cell, comprising contacting the cell with a Y1 transformed
CC cell with the above vector (Y1-EV1); (4) a method for delivering a
CC heterologous protein into a eukaryotic cell, comprising contacting the
CC cell with a Y1 transformed with the above vector (Y1-EV1); (5) a method
CC for inducing an immune response specific for a heterologous protein; (6)
CC a method for inducing a cytotoxic T-lymphocyte (CTL) response specific
CC for a heterologous protein; (7) a method for determining the efficacy of
CC an antigen vaccination regimen in a subject. Y1 is used to treat a
CC pathological disorder, by providing recombinant Yersinia for the safe
CC delivery of proteins into eukaryotic cells. AAV33147-Y33178 are
CC human-derived peptides used to illustrate the method of the invention.
XX
SQ Sequence 9 AA;

Query Match 91.4%; Score 53; DB 20; Length 9;
 Best Local Similarity 88.9%; Pred. No. 3.4e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Caps 0;

OY 1 KTWGQYNAV 9
 Db 1 ktwgqywav 9

RESULT 13

AAV40211
 ID AAV40211 standard; Peptide: 9 AA.

AC AAV40211;

DT 19-NOV-1999 (first entry)

DE Amino acid sequence of a human melanoma epitope.

XX Cytotoxic T cell; T lymphocyte; CD8+ epitope; T helper cell;

KW CD4+ epitope; B epitope; lipopeptide; interferon gamma; adjuvant;

KW vaccine; tumor; infection; immune response; cytokine profile;

KW acquired immune deficiency syndrome; papilloma; cancer; hepatitis;

KW autoimmune disease.

XX Homo sapiens.

PN FR2774687-A1.

PD 13-AUG-1999.

PF 06-FEB-1998; 98FR-0001439.

PR 06-FEB-1998; 98FR-0001439.

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

PA (INSP) INST PASTEUR LILLE.

PI Thiam K, Guillet JG, Ver Waerde C, Aurlaut C, Gras MH, Lohng E;

DR WPI; 1999-510734/43.

PT New lipopeptide comprising C-terminal interferon-gamma fragment with
 attached lipophilic groups, used as interferon mimic, e.g. for treating
 cancer or virus infection

PS Disclosure; Page 35; 53pp; French.

XX AAV40123-Y40379 represent epitopes that are able to activate cytotoxic
 CC T lymphocytes (CD8+ epitopes), T helper cells (CD4+ epitopes), or
 CC B epitopes recognized by corresponding antibodies. The epitopes may be
 CC used in the composition of the invention. The specification describes a
 CC lipopeptide that has a peptide part derived from mammalian interferon
 CC gamma (IFN γ) and one or more lipophilic parts comprising a linear or
 CC branched, (un)saturated 4-20C hydrocarbon chain or a steroid. The
 CC lipopeptide mimics the activity of IFN γ . Compositions comprising the
 CC lipopeptide are used to treat or prevent any condition that responds
 CC to IFN γ , and as adjuvant for vaccines (particularly those directed
 CC against tumors, viral or parasitic infections), to stimulate or
 CC (re)orient the immune response between types 1 and 2 cytokine profiles.
 CC Particular applications are treatment of infections (particularly
 CC viral, e.g. acquired immune deficiency syndrome, papilloma (cancer) and
 CC hepatitis, but also bacterial, fungal, parasitic or helminth); cancers
 CC (particularly of kidney, cutaneous T cells or ovary, chronic
 CC myelogenous leukemia or mesothelioma), allergy; and autoimmune
 CC diseases.

XX Sequence 9 AA;

Query Match 91.4%; Score 53; DB 20; Length 9;

Best Local Similarity 88.9%; Pred. No. 3.4e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Caps 0;

OY 1 KTWGQYNAV 9
 Db 1 ktwgqywav 9

RESULT 14

AAV26867
 ID AAV26867 standard; peptide: 9 AA.

AC AAV26867;

DT 14-SEP-1999 (first entry)

DE Melanoma-derived lipopeptide epitope #8 for mixed micelles.

XX Micelle; microaggregate; induction; immune response; lipopeptide; CTL;

KW cytotoxic T-lymphocyte; epitope; lipid; helper T-lymphocyte; HTL; HBV;

KW tetanus; toxin; vaccine; HIV; hepatitis B virus; papilloma virus; p53;

KW melanoma; Plasmodium falciparum; malaria.

XX Synthetic.

OS Homo sapiens.

PN FR2771640-A1.

PD 04-JUN-1999.

PF 03-DEC-1997; 97FR-0015246.

PR 03-DEC-1997; 97FR-0015246.

PA (CNRS) CNRS CENT NAT RECH SCI.

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

PA (INSP) INST PASTEUR LILLE.

PI Bossus M, Bourgault VI, Gras-Masse H, Guillet JG, Lippens G;

PI Tartar A, Wlarszeski JM;

DR WPI; 1999-349509/30.

PT Immunogenic lipopeptide micelles - comprising lipopeptides
 PT containing cytotoxic and helper T-lymphocyte epitopes

PS Disclosure; Page 37; 60pp; French.

XX The invention relates to the generation of mixed micelles or
 CC microaggregates for inducing an immune response comprise: (a) a first
 CC lipopeptide comprising at least one CTL (cytotoxic T-lymphocyte) epitope
 CC and at least one lipid unit; and (b) a second lipopeptide comprising at
 CC least one HTL (helper T-lymphocyte) epitope and at least one lipid unit
 CC different from that of the first lipopeptide. This peptide represents
 CC an example of a lipopeptide epitope used in the invention and is derived
 CC from a human melanoma protein. The immunogenic lipopeptide micelles
 CC are used in vaccines, especially against HIV, hepatitis B virus (HBV),
 CC papilloma viruses, p53, melanoma or Plasmodium falciparum malaria.

XX Sequence 9 AA;

Query Match 91.4%; Score 53; DB 20; Length 9;
 Best Local Similarity 88.9%; Pred. No. 3.4e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Caps 0;

OY 1 KTWGQYNAV 9
 Db 1 ktwgqywav 9

RESULT 15

AAV01753

ID	AAV01753	standard; Peptide; 9 AA
XX		
AC	AAV01753;	
XX		
DT	25-JUN-1999	(first entry)
XX		
XX		Exemplary antigenic peptide derived from gp100(pmel117).
DE		
XX		MAGE-3; tumour associated gene; human leucocyte antigen Class II;
KM		autologous CM4+ cell; MAGE-3 related disease; cancer; melanoma;
KM		osteosarcoma; leukemia; carcinoma.
XX		
OS	Homo sapiens.	
XX		
PN	W09914326-A1.	
XX		
PD	25-MAR-1999.	
XX		
PF	04-SEP-1998;	98WO-US18601.
XX		
PR	12-SEP-1997;	97US-0928615.
XX		
XX		
PA	(LUDM-) LUDMIG INST CANCER RES.	
XX	(UYVR-) UNIV VRIJE BRUSEL.	
PI	Boon-Falleur T, Chaux P, Corthals J, Heirman C;	
PI	Luiten R, Stroobant V, Thielemans K, Van Der Bruggen P;	
XX		
DR	WPI: 1999-244031/20.	
XX		
FT	Isolated peptides that bind to human leucocyte antigen class II	
PT	molecules	
XX		
PS	Disclosure; Page 29; 88pp; English.	
XX		
CC		The present sequence represents an exemplary tumour associated peptide
CC		antigen. The specification describes a MAGE-3 tumour associated gene.
CC		Peptides (AAV01721-75) that bind human leucocyte antigen (HLA) Class II
CC		molecules can be derived from the MAGE-3 protein. These peptides and
CC		autologous CM4+ cells that bind to a complex of MAGE-3 peptide
CC		and HLA Class II, are used to treat MAGE-3 related diseases,
CC		particularly cancers (e.g. melanoma, osteosarcoma, leukemia and
CC		various forms of carcinoma). The peptides are also used to produce
CC		specific antibodies. Detection of the peptides, e.g. in binding
CC		assays, particularly with antibodies, is used for diagnosis of such
CC		diseases.
XX		
XX		
SQ	Sequence	9 AA;
	Query Match	91.4%; Score 53; DB 20; Length 9;
	Best Local Similarity	86.9%; Pred. No. 3.4e+05;
	Matches	8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 KTWGQYNAV 9	
	1 ktwgqyqyv 9	
DB		
RESULT	16	
AAV00715		
ID	AAV00715	standard; peptide; 9 AA.
XX		
AC	AAV00715;	
XX		
DT	12-MAY-1999	(first entry)
XX		
DE		Tumour antigen booster peptide gp100Pmel117 HLA-A2 #1.
XX		
XX		Tumour antigen; booster peptide; immune response modulation; allergy;
KM		immune response enhancer; tumour cell; tumour rejection antigen;
KM		leukocyte antigen-presenting molecule; autoimmune disease;
KM		allograft rejection.

XX	OS	Homo sapiens.
XX	XX	
XX	FN	W09858956-A2.
XX	PD	30-DEC-1998.
XX	PF	19-JUN-1998; 98WO-US12894.
XX	FR	23-JUN-1997; 97US-0880979.
XX	PA	(LUDW-). LUDWIG INST CANCER RES.
XX	PI	Boon-Falleur T, Uyttenhove C, Warner G;
XX	DR	WPL: 1999-105612/09.
XX	PT	Immunization methods using viruses expressing antigen for priming
XX	PT	and booster immunizations - useful for modulating immune responses
XX	PT	against antigen, e.g. enhancing immune response against tumour cells
XX	PS	expressing tumour rejection antigens
XX	PS	Disclosure: Page 10; 33pp; English.
XX	AX	This sequence represents a tumour antigen booster peptide that can be
CC	CC	used in the method of the invention. The method is for modulating an
CC	CC	immune response in a mammal against an antigen, and comprises:
CC	CC	(A) inducing an immune response by: (i) administering a virus containing
CC	CC	a nucleic acid molecule encoding the antigen or its precursor to generate
CC	CC	an immune response; and (ii) administering at least one booster dose
CC	CC	comprising a peptide including the antigen, in an adjuvant, in a combined
CC	CC	amount effective to enhance the initial immune response; or
CC	CC	(B) reducing an immune response as defined for (A) but using a
CC	CC	non-adjuvant with the peptide which includes the antigen, in an amount
CC	CC	effective to reduce the initial immune response. Method (A) is used to
CC	CC	enhance the immune response against tumour cells expressing tumour
CC	CC	rejection antigen, and against pathogens in subjects having human
CC	CC	leukocyte antigen-presenting molecules. Method (B) is used to reduce the
CC	CC	immune response in allergy, autoimmune disease, and allograft rejection.
CC	CC	Method (A) provides an immunisation method which, unlike prior art, is
XX	XX	not limited by the host immune response against viral vectors.
XX	SQ	Sequence 9 AA:
OY	DB	Query Match 91.4%; Score 53; DB 20; Length 9; Best Local Similarity 88.9%; Pred. No. 3.4e+05; Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0. 1 KTWGQYMAV 9 1 ktwgqywav 9
RESULT 17	ID	AAI10449 standard; Peptide: 9 AA.
XX	AC	AAI10449;
XX	DT	12-MAY-1999 (first entry)
XX	DE	HLA Class I motif peptide SEQ ID NO:379.
XX	KW	Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system;
XX	KW	immunisation; tumour; infectious disease; immunotherapy; cancer;
XX	XX	malignant melanoma; viral disease; hepatitis; AIDS.
XX	OS	Synthetic.
XX	OS	Homo sapiens.
XX	XX	
XX	XX	W09902183-A2

XX	PD	21-JAN-1999.
XX	PF	10-JUL-1998;
XX	PF	98WO-US14289.
XX	PR	10-DEC-1997;
XX	PR	97US-0988320.
XX	PR	10-JUL-1997;
XX	PR	97CA-2209815.
XX	PA	(CTLI-) CTL IMMUNOTHERAPIES CORP.
XX	PI	Kuendig TM, Sismard JUL;
XX	PI	WPI; 1999-120514/10.
XX	PT	Inducing a cytotoxic T lymphocyte response - by maintaining a level
XX	PT	of antigen in the lymphatic system of a mammal so as to provide a
XX	PT	sustained CTL response, used to treat, e.g. AIDS
XX	PS	Disclosure; Page 40; 199pp; English.
XX	CC	The present invention describes a method of inducing and/or sustaining
XX	CC	an immunological cytotoxic T lymphocyte (CTL) response in a mammal. The
XX	CC	method comprises: (a) delivering an antigen to the mammal at a level to
XX	CC	induce an immunological CTL response in the mammal; and (b) maintaining
XX	CC	the level of the antigen in the mammal's lymphatic system to deliver in
XX	CC	the immunologic CTL response. The method can be used for the delivery of
XX	CC	e.g. a differentiation antigen, a tumour-specific multilineage antigen,
XX	CC	an embryonic antigen, an oncogene antigen, a mutated tumour-suppressor
XX	CC	gene antigen, or a viral antigen. They can be used for the treatment of
XX	CC	disease such as cancer, e.g. malignant melanoma or infectious disease,
XX	CC	e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery
XX	CC	to the lymphatic system provides for potent CTL stimulation that takes
XX	CC	place in the milieu of the lymphoid organ, and it sustains stimulation
XX	CC	that is necessary to keep CTL active, cytotoxic and recirculating
XX	CC	through the body. AAY10071 to AAY10639 represent examples of peptide
XX	CC	antigens given in the present invention.
XX	Sequence	9 AA:

```

Query Match          91.4%: Score 53: DB 20: Length 9;
Best Local Similarity 88.9%: Pred. No. 3.4e+05;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      1 KTWGQYMAV 9
        ||||| 1
Db      1 ktwgqyqv 9

RESULT 18
AAB33662
ID AAB33662 standard; Peptide: 9 AA.
XX
XX AAB33662;
XX AC
XX DT
XX XX
XX XX
DE MHC class I associated immunogenic peptide SEQ ID 61.
XX
XX Microparticle; nucleic acid delivery; immunogenic peptide; MHC I; MHC II;
XX major histocompatibility complex; vaginal tissue; mucosal tissue..
XX OS
XX Unidentified.
XX
XX WO200053161-A2.
XX PN
XX PD
XX 14-SEP-2000.
XX
XX 10-MAR-2000; 2000WC-US06578.
XX PF
XX 11-MAR-1999; 99US-0266463.
XX PR 27-MAY-1999; 99US-0321346.
XX
XX (ZYCO-) ZYCOS INC.

```

PI Lunsford LB, Putnam D, Hedley ML;
 XX
 XX WPI: 2000-638130/61.
 XX
 XX Microparticles useful for administering a nucleic acid into the mucosal
 PT tissue preferably vaginal tissue of an animal, comprises a polymeric
 PT matrix, a lipid and a nucleic acid molecule
 XX
 PS Disclosure: Page 14; 96pp; English.
 XX
 CC The present invention relates to microparticles which are less than 20
 CC microns in diameter, which comprise a polymeric matrix, a lipid and a
 CC nucleic acid molecule. The microparticle is specifically not
 CC encapsulated in a liposome and does not comprise a cell. The nucleotide
 CC histone encodes an expression product that binds to major
 CC histocompatibility complex (MHC) type I or II molecules. Peptides
 CC AA833602-833647 represent MHC class II associated immunogenic peptides,
 CC and AA833648-833710 represent MHC class I associated immunogenic
 CC peptides. The peptides are examples of the expression products of the
 CC nucleotide sequences which can be included in the microparticles of the
 CC invention. Sequences AA83711-83716 represent alternative expression
 CC products and nuclear localisation signals also used in the invention. The
 CC microparticles are useful for administering a nucleic acid into the
 CC mucosal tissue preferably vaginal tissue of an animal.
 XX
 XX Sequence 9 AA:
 X0

Query Match	91.4%	Score 53	DB 21	Length 9
Best Local Similarity	88.9%	Pred. No. 3.4e+05		
Matches	8	Conservative	0	Mismatches 1
			Indels	0
			Gaps	0

OY	1	KTWGQYNAV	9
			1
Db	1	ktwgqyngv	9

RESULT	19
AAAB23679	
ID	AAAB23679 standard; Peptide: 9 AA.
XX	
AC	AAAB23679;
XX	
DT	05-JAN-2001 (first entry)
XX	
DE	Cytotoxic T Lymphocyte (CTL) epitope SEQ ID NO:31.
XX	
KW	ATrase: Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;
KW	Immune response; infectious disease; malaria; cytotoxic T cell;
KW	Cytostatic; immunostimulant; cellular immune response inducer;
KM	protozoacide; leukaemia; cancer.
XX	
OS	Homo sapiens.
XX	
PN	WO200049041-A1.
XX	
PD	24-AUG-2000.
XX	
PF	18-FEB-2000; 2000WO-JP00941.
XX	
PR	19-FEB-1999; 99JP-0041535.
XX	
RA	(SUME) SUMITOMO ELECTRIC IND CO.
XX	
PI	Shinbara N, Uono H, Yui K;
XX	
DR	WPI: 2000-543748/49.
XX	
PT	Fused protein capable of inducing cellular immune response, useful as
XX	active ingredient for drug compositions in preventing and/or treating
PT	infectious diseases such as malaria or cancer
XX	

PS Claim 7; Page 58; 72pp; Japanese.

CC The present invention describes a fused protein (I) prepared from a
CC peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by
CC cytotoxic T cells and a protein containing the ATPase domain of a heat
CC shock protein. Also described are: (1) a drug composition containing (I)
CC as active ingredient; (2) a DNA encoding (I); (3) an expression vector
CC containing the DNA of (2); and (4) a transformant which can retain the
CC expression vector of (3). (I) has cytostatic, immunostimulant and
CC protozoacide activities, and can be used as a cellular immune response
CC inducer. The protein is useful as an active ingredient for drug
CC compositions in preventing and/or treating infectious diseases such as
CC malaria or cancer e.g. to provide systemic immunity against leukaemia.
CC The present sequence represents a specifically claimed CTL epitope
CC for use in a fused protein of the present invention.

XX SQ Sequence 9 AA;

Query Match 91.4%; Score 53; DB 21; Length 9;
Best Local Similarity 88.9%; Pred No. 3.4e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYMAV 9
| | | | | | |
Db 1 ktwgywqv 9

RESULT 20
AAB08694
ID AAB08694 standard; Peptide; 9 AA.

XX AAB08694;
XX
XX
XX 02-JAN-2001 (first entry)

DE Antigenic peptide from tumour rejection antigen gp100(Pmel117).

XX
XX
XX Epha3; HLA class II-binding peptide; human leukocyte antigen; antigen;
XX CD4+ T lymphocyte; tumour associated gene; vaccine.

OS Homo sapiens.

XX
XX
XX WO200050589-A1.
XX
XX
XX 31-AUG-2000.
XX
XX
XX 18-FEB-2000; 2000WO-US04326.
XX
XX
XX 22-FEB-1999; 99US-0121170.
XX
XX
XX 08-OCT-1999; 99US-0158566.
XX
XX
XX (LUDW-) LUDWIG INST CANCER RES.

PI Chiari R, Coulie P, Boon-Falleur T;
XX
XX
XX WPI: 2000-572089/53.
XX
XX
XX Novel tyrosine kinase receptor. Epha3 human leukocyte antigen (HLA)
XX class II binding peptide and nucleic acid encoding the receptor, useful
XX for diagnosing and treating conditions characterized by expression of
XX Epha3 gene -

PS Disclosure; Page 35; 107pp; English.

XX AAB0868-B08704 represent antigenic peptides characteristic of tumours.
CC The peptides may be combined in vaccines with a human Epha3 HLA (human
CC leukocyte antigen) class II-binding peptide. Epha3 antigens, when
CC presented by an antigen presenting cell having a HLA class II molecule,
CC effectively induce activation and proliferation of CD4+ T lymphocytes.
CC Epha3 is a tumour associated gene. Epha3 HLA binding peptides are used
CC for selectively enriching a population of T lymphocytes. The peptides
CC are also used for diagnosing a disorder characterized by Epha3 or Epha3

CC HLA binding peptide expression. The peptides are also used to treat a
CC disorder characterized by Epha3 expression. The Epha3 binding peptides
CC are useful in producing vaccines and antibody.

XX SQ Sequence 9 AA;

Query Match 91.4%; Score 53; DB 21; Length 9;
Best Local Similarity 88.9%; Pred No. 3.4e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYMAV 9
| | | | | | |
Db 1 ktwgywqv 9

RESULT 21
AAV71520
ID AAV71520 standard; peptide; 9 AA.

XX AAV71520;
XX
XX
XX 12-OCT-2000 (first entry)

DE Human gp100 Pmel117 nonapeptide-1.

XX
XX
XX
XX gp100 Pmel117; human; Tumour Rejection Antigen; TRA; tumour; cancer;
XX HLA; Human Leucocyte Antigen; MHC; Major Histocompatibility Complex; CTL;
XX cytolytic T-lymphocyte; immune response stimulator; prophylaxis; therapy;
XX diagnosis; TNF; tumour necrosis factor; vaccine; cytostatic.

OS Homo sapiens.

XX
XX
XX WO200032769-A2.
XX
XX
XX 08-JUN-2000.
XX
XX
XX 26-NOV-1999; 99WO-IB02018.
XX
XX
XX 27-NOV-1998; 98GB-0026143.
XX
XX
XX (LUDW-) LUDWIG INST CANCER RES.

PI Huang L, Van Pel A, Brasseur F, De Plaen E, Boon T;
XX
XX
XX WPI: 2000-412317/35.
XX
XX
XX Novel polypeptides expressed in tumor cells useful for treating cancers
XX have an ability to complex with a major histocompatibility complex
XX molecule and comprises a specific unbroken amino acid sequence -

PS Disclosure; Page 20; 80pp; English.

XX The patent discloses MAGE-A10 and MAGE-A8 polypeptide, nonapeptide and
CC decapeptide sequences, that function as tumour rejection antigens
CC (TRAS). These peptides are capable of forming a complex with major
CC histocompatibility complex (MHC) molecule type HLA-A2.1 (Human Leucocyte
CC Antigen), that are recognised by T-lymphocytes and elicit an immune
CC response from cytolytic T-lymphocytes (CTL). They function as an immune
CC response stimulator. Tumour rejection antigens are useful in prophylaxis,
CC therapy and diagnosis of tumours and are effective in controlling or
CC preventing tumour growth. The present sequence is the human gp100 Pmel117
CC nonapeptide-1, that corresponds to residues 154-162 of the tumour
CC associated gene, gp100 Pmel117 encoding protein. It can be administered
CC to induce or enhance an immune response and is presented by HLA-A2
CC complex. This peptide can serve as a tumour rejection antigen (TRA) and
CC in combination with adjuvants, can produce vaccines useful for treating
CC a variety of tumours.

XX SQ Sequence 9 AA;

Query Match 91.4%; Score 53; DB 21; Length 9;

Best Local Similarity 88.9%; Pred. No. 3.4e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYNAV 9
| | | | | | |
Db 1 ktwgqywgqv 9

RESULT 22

AAB02622
ID AAB02622 standard; Peptide: 9 AA.

AC AAB02622;

DT 18-AUG-2000 (first entry)

DE Tumour associated peptide antigen from gp100 #2.

KW MAGE-A3; HLA class II; human leukocyte antigen; antibody; vaccine;
cancer; human; tumour; tumour associated gene product.

OS Homo sapiens.

PN MO200020581-A1.

PD 13-APR-2000.

PF 15-SEP-1999; 99WO-US21230.

PR 05-OCT-1998; 98US-0166448.

PA (LUDM-) LUDWIG INST CANCER RES.

(UYVR-) UNIV VIRGE BRUSSEL.

PI Chaux P, Stroobant V, Boon-Falleur T, Van Der Bruggen P;
Schultz ES, Van Snick J, Lethé B, Thielemans K, Corthals J;

PI Heirman G;

DR WPI: 2000-317713/27.

XX New MAGE-A3 class II binding peptides, useful to diagnose and treat
PT tumours, are fragments of MAGE-A3 which bind to and are presented to T
PT lymphocytes by human leukocyte antigen class II molecules -
XX
PS Disclosure: Page 33; 11pp; English.

XX The present invention relates to MAGE-A3 (tumour associated gene
CC product) human leukocyte antigen (HLA) class II-binding peptides (see
CC AAB02626-802395, and AAB02633-802637). These peptides are presented to T
CC cells in the context of HLA class II molecules. The peptides stimulate
CC the activity and proliferation of CD4+ T lymphocytes. The invention also
CC includes nucleotide sequences encoding MAGE-3A peptides (see AAA37928
CC and AAA37938-A37940). The peptides and nucleotide sequences can be used
CC to create antibodies against the MAGE-A3 peptides, the antibodies,
CC peptides and nucleotide sequences can be used to create a vaccine. The
CC peptides are used to diagnose or treat a disorder characterized by
CC expression of MAGE-3, particularly cancer. The methods can also be used
CC in the diagnosis of disorders associated with MAGE-3 expression. Included
CC in the invention are other human tumour antigens (see AAB02596-802637),
CC and PCR primers used in the course of the invention (see AAA37929-A37937
CC and AAA37941-A37942).

XX Sequence 9 AA:

Query Match 91.4%; Score 53; DB 21; Length 9;

Best Local Similarity 88.9%; Pred. No. 3.4e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYNAV 9
| | | | | | |
Db 1 ktwgqywgqv 9

RESULT 23

AAV90803
ID AAV90803 standard; peptide: 9 AA.

AC AAV90803;

DT 25-AUG-2000 (first entry)

DE Human leukocyte antigen A2 gp100-Pmel117 peptide SEQ ID NO:32.

KW Human leukocyte antigen; HLA-B35; binding; recognition; lysis;
cytolytic T cell; tyrosinase; immune response; diagnosis;

KW identification; human.

OS Homo sapiens.

PN MO200021551-A1.

PD 20-APR-2000.

PF 04-OCT-1999; 99WO-US23038.

PR 09-OCT-1998; 98US-0169717.

PA (LUDM-) LUDWIG INST CANCER RES.

PI Ooms A, De Giovanni G, Morel S, Van Den Eynde B, Boon-Falleur T;

DR WPI: 2000-317842/27.

XX Isolated peptides, sometimes derived from tyrosinase, which bind to
PT HLA-B35 leading to recognition and lysis of the resulting complexes by
PT cytolytic T cells -
XX

PS Example 3; Page 9; 20pp; English.

XX The present invention describes isolated peptides which bind to human
CC leukocyte antigen (HLA)-B35 molecules leading to recognition and lysis
CC of the resulting complexes by cytolytic T cells. The isolated peptides
CC are sometimes derived from tyrosinase. Compositions comprising the
CC peptides of the invention can be used to generate immune responses,
CC preferably in humans, but also in non-human animals to generated immune
CC components which can then be used to treat humans or diagnostically.
CC Therapeutically, the peptides are useful in generation of cytolytic T
CC cells either in vitro or in vivo which specifically lyse pathogenic
CC cells. The peptides can also be used to identify HLA-B35 positive
CC cells, or to remove HLA-B25 positive cells from mixtures containing
CC such cells. Nucleic acid molecules encoding the peptides can be used
CC inter alia as probes to identify cells which are expressing tyrosinase.
CC The present sequence represents an HLA binding peptide used in the
CC exemplification of the present invention.

XX Sequence 9 AA:

Query Match 91.4%; Score 53; DB 21; Length 9;

Best Local Similarity 88.9%; Pred. No. 3.4e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYNAV 9
| | | | | | |
Db 1 ktwgqywgqv 9

RESULT 24

AAV92299
ID AAV92299 standard; peptide: 9 AA.

AC AAV92299;

DT 10-AUG-2000 (first entry)

Tumour associated disorders (e., endogenous retrovirus mediated tumours, especially melanomas) can be treated or ameliorated by administering antitense nucleic acid to reduce the expression of tumour associated genes such as HERV-AVL3-B. Progression of a disorder characterized by the expression of the HERV-AVL3-B endogenous retrovirus tumor rejection antigen (ERRA) can be diagnosed or monitored by contacting a non-testis biological sample with an agent that binds to the complex and determining the interaction. A disorder can also be treated by administering an agent that enriches the presence of HLA and HERV-AVL3-B ERRA or by administering autologous cytotoxic T-cells sufficient to ameliorate the disorder. Fragments of the HERV-AVL3-B coding sequence are useful as probes or amplification primers for determining the expression of HERV-AVL3-B genes, to express tumor associated polypeptides in vivo and in vitro and to prepare fragments of such polypeptides to synthesize antibodies. Antigenic peptides of HERV-AVL3-B can be useful for generating antibodies either alone or as fusion proteins, as components of immunoassay and for determining the binding specificity of HLA molecules and/or cytotoxic T lymphocyte (CTL) for HERV-AVL3-B proteins. Peptides derived from the HERV-AVL3-B coding sequence and which are presented by MHC molecules and recognised by CTL or helper T-lymphocytes can be combined with peptides from other tumour rejection antigens by preparation of hybrid nucleic acids or polypeptides to produce polypeptides. This exemplary tumour associated peptide antigen corresponds to amino acids 154-162 of the gp100(pmel17) polypeptide. See also AA782953-Y82986.

Qy	1	KTWGOYMAV	9
	1		1
Db	1	KTWgqywgV	9

KW	immune response; cancer; tyrosinase; tumour rejection antigen;
KW	major histocompatibility complex.
XX	
XX	Synthetic.
OS	Homo sapiens.
XX	
PN	W09950637-A2.
XX	
PD	07-OCT-1999.
XX	
PF	25-MAR-1999; 99WO-US06615.
XX	
PR	27-MAR-1998; 98US-0049850.
XX	
PA	(LUDWIG) LUDWIG INST CANCER RES.
XX	(UYOX-) UNIV OXFORD.
PI	Romero P, Dunbar R, Valmori D, Ogg G, Cerrotini J, Cerundolo V;
DR	WPI; 2000-052636/04.
XX	
PT	New isolated complex of binding partners and immune complexes
PT	containing major histocompatibility molecules and peptide, used to
PT	isolate and detect cytotoxic T cells, particularly directed against
PT	cancer -
XX	
XX	Example 50; Page 64; 91pp; English.
XX	
CC	The present invention describes an isolated complex (A) comprising: (i)
CC	first and second binding partners (BP1, BP2); and (ii) several immune
CC	complexes (IC) containing a major histocompatibility complex (MHC)
CC	molecule (I), a beta2-microglobulin molecule (b2MG) and a peptide (II)
CC	that binds specifically to (I). (A) are used for analysis of cytolytic
CC	T cells (CTL) for characterisation of an immune response to tumours or
CC	for monitoring vaccine trials. Particularly they are used to isolate or
CC	detect particular CTL (especially those in tumour-infiltrated lymph
CC	nodes), including visualisation of antigen-specific CTL and determination
CC	if the cells have been activated by in vivo exposure to antigen. Isolated
CC	precursor cells may be expanded in vitro to produce cells with high
CC	tumouricidal activity, for therapeutic or diagnostic use. A method for
CC	the present invention allows: (i) preselection of T cell clones for use
CC	in immunotherapy according to their homing molecules; and (ii) improves
CC	the lytic activity of T cells populations by inhibition of natural
CC	killer cell receptors. The present sequence represents a peptide
CC	used in the exemplification of the present invention.
XX	
XX	Sequence 9 AA;
XX	
XX	Query Match 91.4%; Score 53; DB 21; Length 9;
XX	Best Local Similarity 88.9%; Pred. No. 3.4e+05;
XX	Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY	1 KTWGQYNAV 9
DB	1 KTWGQYNAV 9
XX	
XX	RESULT 28
XX	AAB31354
ID	AAB31354 standard; peptide; 9 AA.
XX	
XX	AAB31354;
XX	
DT	20-APR-2001 (first entry)
XX	
DE	Exemplary antigen characteristic of tumours, derived from gp100.
XX	
XX	MAGE-A1; HLA: human leukocyte antigen; CD4+ T lymphocyte; cancer;
KW	MAGE-A1 HLA class II-binding protein; vaccine.
XX	
XX	Homo sapiens.
XX	

PN WO200078806-A1.
 XX 28-DEC-2000.
 XX 14-JUN-2000; 2000MO-US16287.
 PF 18-JUN-1999; 99US-0336091.
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA Van Snick J, Lethe B, Chaux P, Boon-Falleur T, Van Der Bruggen P;
 PI WPI, 2001-102698/11.
 DR Novel MAGE-A1 human leukocyte antigen class II peptides which bind to
 XX and are presented to the class II molecules, useful for inducing immune
 PT response and treating cancers characterized by expression of MAGE-A1 -
 XX
 PS Disclosure: Page 33; 78pp; English.
 CC AAB31302-59 represent exemplary antigens which are characteristic
 CC of tumours. They can be used to enhance the immune response of vaccines
 CC comprising peptides derived from human MAGE-A1 HLA (human leukocyte
 CC antigen) class II-binding protein. Peptides derived from the MAGE-A1 HLA
 CC binding protein stimulate the activity and proliferation of CD4+ T
 CC lymphocytes. The MAGE-A1 HLA binding protein is useful as a diagnostic
 CC agent for diagnosing a disorder characterized by expression of MAGE-A1.
 CC The protein is used for treating a disorder characterized by expression
 CC of MAGE-A1 such as cancers e.g. melanoma, squamous cell carcinomas,
 CC colorectal carcinomas, osteosarcomas, and lymphocytic leukemias.
 CC Peptides derived from the MAGE-A1 HLA binding protein are useful in the
 CC production of anti-tumour vaccines.
 CC
 XX Sequence 9 AA;
 SQ

Query Match 91.4%; Score 53; DB 22; Length 9;
 Best Local Similarity 88.9%; Pred. No. 3.4e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYWAY 9
 | | | | | | | |
 Db 1 ktwgqyway 9

RESULT 29
 AAR78643
 ID AAR78643 standard; Protein; 10 AA.
 XX AAR78643;
 AC
 XX 22-JAN-1996 (first entry)
 DT
 XX Immunogenic peptide of melanoma associated antigen gp100.
 DE
 XX Melanoma; antigen; vaccine; immunogen; primer; probe; detection;
 KW identification; tumour; gp100.
 XX
 OS Homo sapiens.
 XX
 PN EP668350-A1.
 PD 23-AUG-1995.
 XX
 PF 14-FEB-1995; 95EP-0200348.
 XX
 PR 21-DEC-1994; 94EP-0203709.
 PR 16-FEB-1994; 94EP-0200337.
 XX
 PA (ALKU) AKZO NOBEL NV.
 XX
 PI Adema GJ, Figdor CG;
 XX

DR WPI, 1995-284790/38.
 DR N-PSDB; AAO96055.
 XX
 PT Melanoma associated antigen gp100 - used in vaccines and for the
 PT detection of tumours
 XX
 PS Claim 5; Page 31; 40pp; English.
 CC Immunogenic peptides derived from the melanoma associated antigen
 CC (see AAR78639-45) may be used in the production of vaccines.
 CC Nucleotide sequences encoding the immunogenic peptides may be used
 CC as primers and probes in the detection of melanoma cells. Tumour
 CC infiltrating lymphocytes capable of binding to the melanoma
 CC associated antigen can be cultured ex vivo and returned to melanoma
 CC particles, and when radiolabelled, they may be used to identify
 CC tumour deposits.
 CC
 XX Sequence 10 AA;
 SQ

Query Match 91.4%; Score 53; DB 16; Length 10;
 Best Local Similarity 88.9%; Pred. No. 0.013;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYWAY 9
 | | | | | | | |
 Db 1 ktwgqyway 9

RESULT 30
 AAR84209
 ID AAR84209 standard; Peptide; 10 AA.
 XX AAR84209;
 AC
 XX 25-APR-1996 (first entry)
 DT
 XX gp100 melanoma antigen immunogenic peptide (G10-154).
 DE
 XX gp100; melanoma antigen recognised by T-cells; MART; melanoma;
 KW metastatic melanoma; tumour-associated antigen;
 KW immunogenic peptide; diagnosis; prognosis; prophylaxis;
 KW therapy; vaccine.
 XX
 OS Synthetic.
 XX
 PN WO9529193-A2.
 PD 02-NOV-1995.
 XX
 PF 21-APR-1995; 95WO-US05063.
 XX
 PR 05-APR-1995; 95US-0417174.
 PR 22-APR-1994; 94US-0231565.
 XX
 PA (USSH) US SEC DEPT HEALTH.
 XX
 PI Kawakami Y, Rosenberg SA;
 XX
 DR WPI, 1995-382963/49.
 XX
 PT DNA encoding melanoma antigens recognised by T-lymphocytes - also
 PT vectors, host cells and antibodies, used to detect, treat and
 PT immunise animal against melanoma.
 XX
 PS Claim 55; Page 131; 184pp; English.
 CC The immunogenic peptide is derived from CDNA25 (AAR84854), a
 CC melanoma antigen derivative of gp100 (see AAR84855). The
 CC peptide and its derivatives (see AAR84200-R84211) are used in
 CC medicaments (vaccines) for the treatment or prevention (by
 CC immunization) of melanoma. Antibodies against melanoma-specific
 CC antigens and its immunogenic peptides may be used in the

CC detection and isolation of the antigen from a sample, the
 CC detection of which is indicative of a disease state
 CC (melanoma or metastatic melanoma).
 XX
 SQ Sequence 10 AA;

Query Match 91.4%; Score 53; DB 16; Length 10;
 Best Local Similarity 88.9%; Pred. NO. 0.013;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KTWGQYNAV 9
 |||||
 Db 1 ktwgqywgq 9

Search completed: July 3, 2001, 10:23:58
 Job time: 1383 sec

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OM protein - protein search, using sw model

Run on: July 3, 2001, 10:28:10 ; Search time 37.77 Seconds
(without alignments)
31.526 Million cell updates/sec

Title: US-09-214-836-9
Sequence: 1 KTWGQYMW 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues
Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP RODENT:*
12: SP_UNCLASSIFIED:*
13: SP_VERTEBRATE:*
14: SP_VIRUS:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	43	72.9	209	2	P73834	P73834 synechocyst
2	41	69.5	73	14	Q9DWM8	Q9DWM8 human papil
3	41	69.5	458	5	O18533	O18533 schistosoma
4	40	67.8	73	14	Q9DWM4	Q9DWM4 human papil
5	40	67.8	281	2	Q9KPY3	Q9KPY3 vibrio chol
6	40	67.8	305	2	Q45818	Q45818 chloroflexu
7	40	67.8	400	2	P74474	P74474 synechocyst
8	40	67.8	498	2	O87798	O87798 pseudomonas
9	40	67.8	501	2	O07068	O07068 burkholderi
10	39	66.1	221	2	Q9K889	Q9K889 streptomyce
11	39	66.1	236	1	Q9RXG5	Q9RXG5 deinococcus
12	39	66.1	276	1	Q9Y9N5	Q9Y9N5 aeropyrum p
13	39	66.1	469	1	O50200	O50200 thermococcu
14	39	66.1	518	5	O02622	O02622 crassostrea
15	38	64.4	160	10	O23952	O23952 gossypium h
16	38	64.4	167	10	Q9XGR7	Q9XGR7 fragaria an
17	38	64.4	169	10	Q9ZP34	Q9ZP34 nicotiana t
18	38	64.4	170	10	Q9SCA6	Q9SCA6 lycopersico
19	38	64.4	191	2	Q9EW89	Q9EW89 streptomyce

20	38	64.4	203	10	O9LIB3	O9LIB3 zinnia eleg
21	38	64.4	228	2	O59962	O59962 streptomyce
22	38	64.4	232	10	P93492	P93492 pinus taeda
23	38	64.4	232	10	P93493	P93493 pinus taeda
24	38	64.4	232	10	P93494	P93494 pinus taeda
25	38	64.4	232	10	P93495	P93495 pinus taeda
26	38	64.4	237	10	O38863	O38863 arabidopsis
27	38	64.4	239	10	O9ZP31	O9ZP31 lycopersico
28	38	64.4	242	10	O9LIB1	O9LIB1 zinnia eleg
29	38	64.4	245	10	O9LIB2	O9LIB2 zinnia eleg
30	38	64.4	245	10	O9FNT1	O9FNT1 cicor arlet
31	38	64.4	246	10	P93442	P93442 oryza sativ
32	38	64.4	247	10	O82625	O82625 lycopersico
33	38	64.4	247	10	O9M517	O9M517 triphysaria
34	38	64.4	248	10	O80622	O80622 arabidopsis
35	38	64.4	249	10	O9ZP36	O9ZP36 nicotiana t
36	38	64.4	249	10	O9ZP35	O9ZP35 nicotiana t
37	38	64.4	249	10	O9M515	O9M515 triphysaria
38	38	64.4	249	10	O9IDR9	O9IDR9 arabidopsis
39	38	64.4	250	10	O39625	O39625 cucumis sat
40	38	64.4	250	10	O9FVG9	O9FVG9 lycopersico
41	38	64.4	251	10	O40636	O40636 oryza sativ
42	38	64.4	252	10	O81133	O81133 prunus arme
43	38	64.4	252	10	O9SD23	O9SD23 regnellidiu
44	38	64.4	252	10	O9FY30	O9FY30 festuca pra
45	38	64.4	252	10	O9FWM2	O9FWM2 prunus avia

ALIGNMENTS

RESULT 1
ID P73834 PRELIMINARY; PRT; 209 AA.
AC P73834;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE HYPOHETICAL 24.5 KDA PROTEIN.
GN SLR2003.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_Taxid=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; Pubmed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Sugitara M., Sasamoto S., Kimura T.,
RA Hosonouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimp S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
DR EMBL: D90910; BAA17891.1; -;
KW Hypothetical protein.
SQ SEQUENCE 209 AA; 24511 MW; 0AA7432F01DD888F CRC64;

Query Match 72.9%; Score 43; DB 2; Length 209;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTWGQYMW 8
Db 75 KTWGQYMW 82
RESULT 2
Q9DWM8 PRELIMINARY; PRT; 73 AA.
ID Q9DWM8;
AC Q9DWM8;

DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE MAJOR CAPSID PROTEIN L1 (FRAGMENT).
 OS Human papillomavirus.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 NCBI_TaxID=10566;
 OX NCBI_TaxID=10566;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FA50;
 RA Antonsson A., Hossain S., Simon M., Hansson B.G.;
 RT "Skin HPV found on foreheads."
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY009882; AAG27044.1; -
 FT NON_TER 1 1
 FT NON_TER 73 73
 SQ SEQUENCE 73 AA; 8479 MW; FID5BC6307D39062 CRC64;

Query Match 69.5%; Score 41; DB 14; Length 73;
 Best Local Similarity 71.4%; Pred. No. 8.5;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 WQGYMOV 9
 DB 42 WGEYWDV 48

RESULT 3
 ID 018533 PRELIMINARY; PRT 458 AA.
 AC 018533;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE PREPROCAPIPSIN C PRECURSOR (EC 3.4.14.1).
 OS Schistosoma japonicum (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
 OC Trematoda; Digenea; Strigeidae; Schistosomatidae; Schistosomatidae;
 OC Schistosoma.
 NCBI_TaxID=6182;
 OX NCBI_TaxID=6182;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CHINESE;
 RX MEDLINE=97442731; PubMed=9297696;
 RA Brindley P.J., Kalina B.H., Dalton J.P., Day S.R., Wong J.Y.,
 RA Smythe M.L., Mcmanus D.P.;
 RT "Proteolytic degradation of host hemoglobin by schistosomes."
 RL Mol. Biochem. Parasitol. 89:1-9(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CHINESE;
 RA Hota-Jamirska L., Dalton J.P., Askov J., Day S.R., Fan J.,
 RA Brindley P.J.;
 RX Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U77932; AAC32040.1; -
 DR HSBP; P00787; ITHE.
 DR InterPro; IPR000169; -
 DR InterPro; IPR000668; -
 DR Pfam; PF00112; Peptidase_C1; 1.
 DR PRINTS; PR00705; PAPA1N.
 DR PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
 DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
 KW Hydroxylase; Signal; Thiol protease.
 FT SIGNAL 1 26 POTENTIAL.
 FT CHAIN 222 458 CATHEPSIN C.
 SQ SEQUENCE 458 AA; 52698 MW; ADA976566C4142C CRC64;

Query Match 69.5%; Score 41; DB 5; Length 458;
 Best Local Similarity 83.3%; Pred. No. 55;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 TWGYW 7
 DB 425 SMGYW 430

RESULT 4
 ID 09DWY4 PRELIMINARY; PRT 73 AA.
 AC 09DWY4;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE MAJOR CAPSID PROTEIN L1 (FRAGMENT).
 OS Human papillomavirus.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 NCBI_TaxID=10566;
 OX NCBI_TaxID=10566;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FA50;
 RA Antonsson A., Hossain S., Simon M., Hansson B.G.;
 RT "Skin HPV found on foreheads."
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY009886; AAG27048.1; -
 FT NON_TER 1 1
 FT NON_TER 73 73
 SQ SEQUENCE 73 AA; 8323 MW; 8A994051AD736407 CRC64;

Query Match 67.8%; Score 40; DB 14; Length 73;
 Best Local Similarity 57.1%; Pred. No. 12;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 WQGYMOV 9
 DB 42 WGEYWDV 48

RESULT 5
 ID 09KPY3 PRELIMINARY; PRT 281 AA.
 AC 09KPY3;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE HYPOTHETICAL PROTEIN VC2229.
 GN VC2229.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-EL TOR N16961 / SEROTYPE O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Ermolaeva M.D., Yamathayan J., Bass S., Qin H., Dragoti I., Sellers P.,
 RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 cholerae."
 RL Nature 406:477-483(2000).
 DR EMBL; AE004294; AAF9373.1; -
 DR TIGR; VC2229; -
 SQ SEQUENCE 281 AA; 31824 MW; 7CA75AD3494FDD0 CRC64;

Query Match 67.8%; Score 40; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 WGOY 7
 Db 99 WGOY 103

RESULT 6

ID 045818 PRELIMINARY; PRT; 305 AA.

AC 045818; 01-NOV-1996 (TREMblrel. 01, Created)

DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)

DE 01-MAR-2001 (TREMblrel. 16, Last annotation update)

GN HYPOTHETICAL 33.7 KDA PROTEIN (BCHGC).

OS BCHGC.

OC Bacteria; Green non-sulfur bacteria; Chloroflexaceae group;

OX NCBI_TaxID=1108;

RP SEQUENCE OF 224-305 FROM N.A.

RC STRAIN-J10-FL;

RX MEDLINE=94192803; PubMed=7511541;

RA Niedermeyer G., Shiozawa J., Lottspeich F., Feick R.;

RT "The primary structure of two chlorosome proteins from Chloroflexus

RT aurantiacus";

RL FRS Lett. 342:61-65(1994).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-J10-FL;

RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=94192803; PubMed=7511541;

RA Niedermeyer G., Shiozawa J.A., Lottspeich F., Feick R.G.;

RT "The primary structure of two chlorosome proteins from Chloroflexus

RT aurantiacus";

RL FRS Lett. 342:61-65(1994).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=20433268; PubMed=10976061;

RA Xiong J., Fischer W.M., Inoue K., Nakahara M., Bauer C.E.;

RT "Molecular evidence for the early evolution of photosynthesis.";

RL Science 289:1724-1730(2000).

DR EMBL: Z34000; CA83965.1; -.

DR EMBL: AF288602; AAG15233.1; -.

DR InterPro: IPR000537; -.

DR Pfam: PF01040; UblA; 1.

KM Hypothetical protein.

SO SEQUENCE 305 AA; 33674 MW; F990F92F2D1C2B07 CRC64;

Query Match 67.8%; Score 40; DB 2; Length 305;
 Best Local Similarity 100.0%; Pred. No. 52;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 WGOY 7

Db 246 WGOY 250

RESULT 7

ID P74474 PRELIMINARY; PRT; 400 AA.

AC P74474; 01-FEB-1997 (TREMblrel. 02, Created)

DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)

DE 01-OCT-2000 (TREMblrel. 15, Last annotation update)

GN D-ALANYL-D-ALANINE CARBOXYPEPTIDASE.

DE SUR1924.

OS Synechocystis sp. (strain PCC 6803).

OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.

OX NCBI_TaxID=1148;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97061201; PubMed=8905231;

RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,

RA Miyajima N., Hirose M., Sugita M., Sasamoto S., Kimura T.,

RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naito K., Okumura S.,

RA Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M.,

RA Tabata S.;

RT "Sequence analysis of the genome of the unicellular cyanobacterium

RT Synechocystis sp. strain PCC6803. II. Sequence determination of the

RT entire genome and assignment of potential protein-coding regions.";

RL DNA Res. 3:109-136(1996).

DR EMBL: D90915; BAA18575.1; -.

DR MEROPS: S12.001; -.

KM Carboxypeptidase.

SO SEQUENCE 400 AA; 44316 MW; 7510481820E462F CRC64;

Query Match 67.8%; Score 40; DB 2; Length 400;
 Best Local Similarity 100.0%; Pred. No. 68;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 WGOY 7

Db 335 WGOY 339

RESULT 8

ID 087798 PRELIMINARY; PRT; 498 AA.

AC 087798; 01-NOV-1998 (TREMblrel. 08, Created)

DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)

DE 01-MAR-2001 (TREMblrel. 16, Last annotation update)

GN TOLUENE, O-XYLENE MONOOXYGENASE OXYGENASE SUBUNIT.

GN TOVA.

OS Pseudomonas stutzeri (Pseudomonas perfectomarina).

OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;

OX Pseudomonas.

NCBI_TaxID=316;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-OX1;

RX MEDLINE=98432776; PubMed=9758777;

RA Bertoni G., Martino M., Galli E., Barbieri P.;

RT "Analysis of the gene cluster encoding toluene/o-xylene monooxygenase

RT from Pseudomonas stutzeri OX1.";

RL Appl. Environ. Microbiol. 64:3626-3632(1998).

DR EMBL: AJ005663; CA06654.1; -.

DR InterPro: IPR003430; -.

DR Pfam: PF02332; Phenol_Hydrox; 1.

KM Monooxygenase.

SO SEQUENCE 498 AA; 57725 MW; E49B0C06D5BB43D8 CRC64;

Query Match 67.8%; Score 40; DB 2; Length 498;
 Best Local Similarity 75.0%; Pred. No. 85;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 TWGQWY 9

Db 368 TWGQWY 375

RESULT 9

ID 007068 PRELIMINARY; PRT; 501 AA.

AC 007068; 01-JUL-1997 (TREMblrel. 04, Created)

DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)

DE 01-MAR-2001 (TREMblrel. 16, Last annotation update)

GN TOLUENE-3-MONOOXYGENASE OXYGENASE SUBUNIT 1.

DE TOLUENE-3-MONOOXYGENASE OXYGENASE SUBUNIT 1.

GN TBHA.
 OS Burkholderia cepacia (Pseudomonas cepacia).
 OC Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
 OC Burkholderia.
 OX NCBI_TaxID=292;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A1;
 RA Ma Y., Herson D.S.;
 RL Submitted (Apr-1997) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF001355; AAB58740.1; -;
 DR InterPro: IPR003430; -;
 DR Pfam: PF02332; Phenol_Hydrolase; 1.
 KW Monooxygenase.
 SQ SEQUENCE 531 AA; 58100 MW; 4AAC6E496C34000 CRC64;

Query Match 67.8%; Score 39; DB 2; Length 501;
 Best Local Similarity 75.0%; Pred. No. 86;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 TWGOYMOV 9
 Db 369 TWGOQMDV 376

RESULT 10
 O9RK89 PRELIMINARY; PRT; 221 AA.
 AC O9RK89;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE PUTATIVE SUBSTRATE BINDING PROTEIN (EXTRACELLULAR) (BINDING-PROTEIN-DEPENDENT TRANSPORT) (FRAGMENT).
 GN SCF1.15.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Seeger K.J., Harris D.;
 RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RX MEDLINE=97000351; PubMed=8843436;
 RA Redenbach M., Kisser H.M., Denapalte D., Eichner A., Cullum J., Kinoshita H., Hopwood D.A.;
 RT "A set of ordered cosmid and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 DR EMBL: AL117323; CAB55535.1; -;
 FT NON_TER 221
 SQ SEQUENCE 221 AA; 24497 MW; D305A7977801DA1C CRC64;

Query Match 66.1%; Score 39; DB 2; Length 221;
 Best Local Similarity 83.3%; Pred. No. 54;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 WGOYMO 8
 Db 73 WMOYMO 78

RESULT 11
 O9RXG5 PRELIMINARY; PRT; 236 AA.
 AC O9RXG5;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE CYTOCHROME C-TYPE BIOGENESIS PROTEIN, HEME EXPORTER PROTEIN C. DR0348.
 GN Deinococcus radiodurans.
 OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
 OX NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-RL;
 RX MEDLINE=20036896; PubMed=10567266;
 RA White O., Eissen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Uitterlinden T., Zaleski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C., Fraser C.M.;
 RT "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";
 RL Science 286:1571-1577(1999).
 DR EMBL: AE001895; AAF09930.1; -;
 DR TIGR: DR0348; -;
 DR InterPro: IPR002541; -;
 DR InterPro: IPR003557; -;
 DR Pfam: PF01578; CytC_asm; 1.
 DR PRINTS: PR01386; CCMCBIOGENSIS.
 SQ SEQUENCE 236 AA; 26591 MW; 18E9BD37E12CE711 CRC64;

Query Match 66.1%; Score 39; DB 2; Length 236;
 Best Local Similarity 83.3%; Pred. No. 57;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TWGOYMO 7
 Db 101 TWGOYMO 106

RESULT 12
 O9Y9N5 PRELIMINARY; PRT; 276 AA.
 AC O9Y9N5;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE 276AA LONG HYPOTHETICAL LACTOSE TRANSPORT SYSTEM PERMEASE PROTEIN. GN APE2253.
 OS Aeropyrum pernix.
 OC Archaea; Crenarchaeota; Desulfurococcales; Desulfurococaceae;
 OC Archaea; Crenarchaeota; Desulfurococcales; Desulfurococaceae;
 OX NCBI_TaxID=56636;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K1;
 RX MEDLINE=99310339; PubMed=10382966;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Adaki A., Kotsugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushiida N., Oguuchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
 RT "Complete genome sequence of an aerobic hyper-thermophilic crenarchaeon, Aeropyrum pernix K1.";
 RL DNA Res. 6:83-101(1999).
 DR EMBL: AP000064; BAA81265.1; -;
 DR InterPro: IPR000515; -;
 DR Pfam: PF00528; BPD_transp; 1.

SEQUENCE 276 AA; 31573 MW; A944BCEBF8032631 CRC64;

Query Match

Best Local Similarity 66.1%; Score 39; DB 1; Length 276;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 KTMGOYMW 9
Db 215 KTMGOYMW 223

RESULT 13

050200

PRELIMINARY; PRT: 469 AA.

AC 050200;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE AMYLASE (EC 3.2.1.1) (ALPHA-AMYLASE) (1,4-ALPHA-D-GLUCAN
GLUCANOHYDROLASE) (GLYCOGENASE).
GN AMY.
OS Thermococcus sp. R3.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Thermococcus.
OX NCBI_TaxID=65421;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RT3;
RL Jones R.A., Patel B., Beacham I.R.;
RA Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOMYDOLYSIS OF 1,4-ALPHA-D-GLUCOSIDIC
LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
DR EMBL: AF017454; AAB87860.1; -
DR HSSP: P06278; 1YUS.
DR InterPro: IPR000461; -
DR Pfam: PF00128; alpha-amylase; 1.
KW Hydrolyase; Glycosidase.
SQ SEQUENCE 469 AA; 52756 MW; C3BD614PBA4DB3E2 CRC64;

Query Match

Best Local Similarity 66.1%; Score 39; DB 1; Length 469;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTMGOYMW 7
Db 204 KSMDOYMW 210

RESULT 14

002622

PRELIMINARY; PRT: 518 AA.

AC 002622;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE ALPHA-AMYLASE PRECURSOR (EC 3.2.1.1) (1,4-ALPHA-D-GLUCAN
GLUCANOHYDROLASE) (GLYCOGENASE) (FRAGMENT).
GN AMY.
OS Crassostrea gigas (Pacific oyster).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;
OC Ostreoida; Ostreidae; Crassostrea.
OX NCBI_TaxID=29159;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-DIGESTIVE GLAND;
RA Moal J., Daniel J.Y., Le Molne S., Sellios D., Van Wormhoudt A.,
RA Samain J.F.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOMYDOLYSIS OF 1,4-ALPHA-D-GLUCOSIDIC
LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
DR EMBL: Y08370; CAA69658.1; -
DR HSSP: P00690; 1JFH.

DR InterPro: IPR000461; -
DR Pfam: PF00128; alpha-amylase; 1.
DR PRINTS: PR00110; ALPHAAMYLASE.
KW Signal; Hydrolyase; Glycosidase.
FT NON_TER 1
FT SIGNAL <1 18
FT CHAIN 19 518 POTENTIAL.
SQ SEQUENCE 518 AA; 57435 MW; 2F3864914E7278AC CRC64;

Query Match
Best Local Similarity 71.4%; Score 39; DB 5; Length 518;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTMGOYMW 7
Db 292 KTMGOYMW 298

RESULT 15

023952

PRELIMINARY; PRT: 160 AA.

AC 023952;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE EXPANSIN (FRAGMENT).
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Malvales; Malvaceae; Gossypium.
OX NCBI_TaxID=3635;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COKER312; TISSUE=COTTON FIBER;
RX MEDLINE=97294938; PubMed=9150611;
RA Shimizu Y.; Aotsuka S., Hasegawa O., Kawada T., Sakuno T., Sakai F.,
RA Hayashi T.;
RT "Changes in levels of mRNAs for cell wall-related enzymes in growing
cotton fiber cells."
RL Plant Cell Physiol. 38:375-378(1997).
DR EMBL: D88415; BAA21109.1; -
DR Mendel: 24197; Goshl:1201;24197.
DR InterPro: IPR000882; -
DR Pfam: PF01357; Pollen-allergen; 1.
DR PRINTS: PR01225; EXPANSINFAMILY.
FT NON_TER 1
SQ SEQUENCE 160 AA; 17672 MW; A7CF0DBDB3B5469D CRC64;

Query Match

Best Local Similarity 64.4%; Score 38; DB 10; Length 160;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 KTMGOYMW 8
Db 110 RNWGOYMW 117

RESULT 16

09XGR7

PRELIMINARY; PRT: 167 AA.

AC 09XGR7;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE EXPANSIN (FRAGMENT).
GN Expi.
OS Fragaria ananassa (Strawberry).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Rosales; Rosaceae; Fragaria.
OX NCBI_TaxID=3747;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. CHANDLER;
RX MEDLINE-97303339; PubMed-9159182;
RA Rose J.K.C., Lee H.H., Bennett A.B.;
RT "Expression of a divergent expansin gene is fruit-specific and
  ripening-regulated."
RL Proc. Natl. Acad. Sci. U.S.A. 94:5955-5960(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. CHANDLER;
RA Rose J.K.C., Lee H.H., Bennett A.B.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. CHANDLER;
RA Rose J.K.C., Lee H.H., Bennett A.B.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF163812; AAD4345.2; -.
DR InterPro; IPR000882; -.
DR Pfam; PF01357; Pollen_allergen; 1.
DR PRINTS; PR01225; EXPANSNFAMILY.
DR ProDom; PD002179; -. 1.
FT NON_TER 1 167
SQ SEQUENCE 167 AA; 17947 MW; A75F1D3C715419E7 CRC64;

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Query Match 64.4%; Score 38; DB 10; Length 167;
Best Local Similarity 62.5%; Pred. No. 58;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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OY 1 KTWGQYMQ 8
DB 160 RNMGQNMQ 167

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RESULT 17
O9P34 PRELIMINARY; PRT; 169 AA.
AC O9P34;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE ALPHA-EXPANSIN PRECURSOR (FRAGMENT).
GN NT-EXP6.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
OC Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. BY2;
RX MEDLINE-99026292; PubMed-9808735;
RA Link B.M., Cosgrove D.J.;
RT "Acid-growth response and alpha-expansins in suspension cultures of
  bright yellow 2 tobacco."
RL Plant Physiol. 118:907-916(1998).
DR EMBL; AF049355; AAC96082.1; -.
DR Mendel; 35959; Nicta1201; 35959.
DR InterPro; IPR000882; -.
DR Pfam; PF01357; Pollen_allergen; 1.
DR PRINTS; PR01225; EXPANSNFAMILY.
FT NON_TER 1 167
SQ SEQUENCE 169 AA; 19000 MW; 312B1F89916662D6 CRC64;

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Query Match 64.4%; Score 38; DB 10; Length 169;
Best Local Similarity 62.5%; Pred. No. 58;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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OY 1 KTWGQYMQ 8

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DB 117 RNMGQNMQ 124

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RESULT 18
O9SCA6 PRELIMINARY; PRT; 170 AA.
AC O9SCA6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE EXPANSIN 18 (FRAGMENT).
GN EXP18.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
OC Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. WEST VIRGINIA 106; TISSUE=FRUIT;
RA Lemaire-Chamley M., Petit J., Causse M., Raymond P., Chevallier C.;
RT "Isolation and characterization of cDNAs expressed during early
  development of tomato fruit by mRNA differential display."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ270960; CAB65694.1; -.
DR InterPro; IPR000882; -.
DR Pfam; PF01357; Pollen_allergen; 1.
DR PRINTS; PR01225; EXPANSNFAMILY.
DR ProDom; PD002179; -. 1.
FT NON_TER 1 170
SQ SEQUENCE 170 AA; 18538 MW; 905131AD9496D17C CRC64;

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Query Match 64.4%; Score 38; DB 10; Length 170;
Best Local Similarity 62.5%; Pred. No. 59;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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OY 1 KTWGQYMQ 8
DB 163 RNMGQNMQ 170

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RESULT 19
O9EW89 PRELIMINARY; PRT; 191 AA.
AC O9EW89;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE BETA-XYLANASE (EC 3.2.1.8) (FRAGMENT).
GN GXN1.
OS Streptomyces olivaceoviridis (Streptomyces corchorus11).
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1921;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-E-86;
RA Bin Y.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-E-86;
RA Zhang H., Yao B., Wang Y.;
RT "Cloning and expression of the 23kD beta-xylanase gene from
  Streptomyces olivaceoviridis E-86."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ292317; CAC19491.1; -.
KW xylan degradation; Hydrolase; Glycosidase.
FT NON_TER 1 191
SQ SEQUENCE 191 AA; 20781 MW; 7E1C45ADE1B6B9C CRC64;

```

Query Match 64.4%; Score 38; DB 2; Length 191;
 Best Local Similarity 66.7%; Pred. No. 66;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTWGQYMW 9
 11:1111

DB 131 KTFNQYMSV 139

RESULT 20
 091LB3 PRELIMINARY; PRT; 203 AA.

ID 091LB3
 AC 091LB3;
 DT 01-OCT-2000 (TREMBREL. 15, Created)
 DT 01-OCT-2000 (TREMBREL. 15, last sequence update)
 DE EXPANSIN (FRAGMENT).
 GN EXPL.

OS zinnia elegans.
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae;
 OC eusteris II; Asterales; Asteraceae; Asteroidae; Heliantheae;
 OC zinnia.
 OX NCBI_TaxID=34245;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-20317189; PubMed-10859177;
 RT "Im K.H., Cosgrove D.J., Jones A.M.;
 "Subcellular localization of expansin mRNA in xylem cells."
 RL Plant Physiol. 123:463-470(2000).
 DR EMBL: AF230331; AAF35900.1; -.
 DR InterPro: IPR000862; -.
 DR Pfam: PF01357; Pollen_allergen; 1.
 DR PRINTS: PR01225; EXPANSINFAMILY.
 DR NON_TER 1
 FT SEQUENCE 203 AA; 22692 MW; 7DC08C7DE9795C16 CRC64;

Query Match 64.4%; Score 38; DB 10; Length 203;
 Best Local Similarity 62.5%; Pred. No. 70;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTWGQYMW 8
 :1111

DB 151 RNWGQNMW 158

RESULT 21
 059962 PRELIMINARY; PRT; 228 AA.

ID 059962
 AC 059962;
 DT 01-NOV-1996 (TREMBREL. 01, Created)
 DT 01-NOV-1996 (TREMBREL. 01, last sequence update)
 DE ENDO-1,4-BETA-XYLANASE (EC 3.2.1.8) (1,4-BETA-D-XYLAN
 XYLANOXYDROLASE).
 GN XYL1.
 OS Streptomyces sp.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomycetes.
 OX NCBI_TaxID=1931;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-538;
 RA Georis J.C.E.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
 CC LINKAGES IN XYLANS.
 CC EMBL: X98518; CAA67143.1; -.
 DR HSSP: P09850; 1XNB.
 DR InterPro: IPR001137; -.

DR Pfam: PF00457; Glyco_hydro.11; 1.
 DR PRINTS: PR00911; GLHYDRLASE11.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW xylan degradation; Hydrolase; Glycosidase.
 FT CHAIN 39 228 ENDO-1,4-BETA-XYLANASE.
 SO SEQUENCE 228 AA; 24493 MW; EAA15233052E74AA CRC64;

Query Match 64.4%; Score 38; DB 2; Length 228;
 Best Local Similarity 66.7%; Pred. No. 79;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTWGQYMW 9
 11:1111

DB 169 KTFNQYMSV 177

RESULT 22
 P93492 PRELIMINARY; PRT; 232 AA.

ID P93492
 AC P93492;
 DT 01-MAY-1997 (TREMBREL. 03, Created)
 DT 01-MAY-1997 (TREMBREL. 03, last sequence update)
 DE EXPANSIN (FRAGMENT).
 OS Pinus taeda (loblolly pine).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=3352;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-HYPOCOTYL.
 RA Hutchinson K.W., Singer P.B., Diaz-Sala C., Greenwood M.S.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U64890; AAB40634.1; -.
 DR Mendel: 12160; Pinata;1201;12160.
 DR InterPro: IPR000882; -.
 DR Pfam: PF01357; Pollen_allergen; 1.
 DR PRINTS: PR01225; EXPANSINFAMILY.
 DR PRINTS: PR00829; LOLPALLERGN.
 DR NON_TER 1
 FT SEQUENCE 232 AA; 24734 MW; 1340AF483DE0741F CRC64;

Query Match 64.4%; Score 38; DB 10; Length 232;
 Best Local Similarity 62.5%; Pred. No. 81;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTWGQYMW 8
 :1111

DB 182 RNWGQNMW 189

RESULT 23
 P93493 PRELIMINARY; PRT; - 232 AA.

ID P93493
 AC P93493;
 DT 01-MAY-1997 (TREMBREL. 03, Created)
 DT 01-MAY-1997 (TREMBREL. 03, last sequence update)
 DE EXPANSIN (FRAGMENT).
 OS Pinus taeda (loblolly pine).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=3352;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-HYPOCOTYL.
 RA Hutchinson K.W., Singer P.B., Diaz-Sala C., Greenwood M.S.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U64891; AAB40635.1; -.
 DR Mendel: 12161; Pinata;1201;12161.

DR InterPro; IPRO00882; -
 DR Pfam; PF01357; Pollen_allergen; 1.
 DR PRINTS; PRO1225; EXPANSNFAMILY.
 DR PRINTS; PRO0829; LOPLIALLERGN.
 FT NON_TER 1
 SQ SEQUENCE 232 AA; 24745 MW; 1340B0573DE907CF CRC64;

Query Match 64.4%; Score 38; DB 10; Length 232;
 Best Local Similarity 62.5%; Pred. No. 81;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 KTWGQYQW 8
 : ||| ||
 Db 182 RNMWGQNMQ 189

RESULT 24
 P93494 PRELIMINARY; PRT; 232 AA.
 AC P93494;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE EXPANSIN (FRAGMENT).
 OS Pinus taeda (loblolly pine).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=3352;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=HYPOCOTYL;
 RA Hutchison K.W., Singer P.B., Diaz-Sala C., Greenwood M.S.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U64892; AAB40636.1; -
 DR Mendel; 12162; Pinta; 1201; 12162.
 DR InterPro; IPRO00882; -
 DR Pfam; PF01357; Pollen_allergen; 1.
 DR PRINTS; PRO1225; EXPANSNFAMILY.
 DR PRINTS; PRO0829; LOPLIALLERGN.
 FT NON_TER 1
 SQ SEQUENCE 232 AA; 24681 MW; 01F29E4E8774F1A0 CRC64;

Query Match 64.4%; Score 38; DB 10; Length 232;
 Best Local Similarity 62.5%; Pred. No. 81;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 KTWGQYQW 8
 : ||| ||
 Db 182 RNMWGQNMQ 189

RESULT 25
 P93495 PRELIMINARY; PRT; 232 AA.
 AC P93495;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE EXPANSIN (FRAGMENT).
 OS Pinus taeda (loblolly pine).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=3352;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=HYPOCOTYL;
 RA Hutchison K.W., Singer P.B., Diaz-Sala C., Greenwood M.S.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U64893; AAB40637.1; -
 DR Mendel; 12163; Pinta; 1201; 12163.
 DR InterPro; IPRO00882; -

DR Pfam; PF01357; Pollen_allergen; 1.
 DR PRINTS; PRO1225; EXPANSNFAMILY.
 DR PRINTS; PRO0829; LOPLIALLERGN.
 FT NON_TER 1
 SQ SEQUENCE 232 AA; 24694 MW; 9238EACD9E1F6C5E CRC64;

Query Match 64.4%; Score 38; DB 10; Length 232;
 Best Local Similarity 62.5%; Pred. No. 81;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 KTWGQYQW 8
 : ||| ||
 Db 182 RNMWGQNMQ 189

RESULT 26
 Q38863 PRELIMINARY; PRT; 237 AA.
 AC Q38863;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE EXPANSIN ATX1 (FRAGMENT).
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96016146; PubMed=7568110;
 RA Sheehy T.Y., Shi J., Durachko D.M., Gullitlan M.J.;
 RA McQueen-Mason S.J., Shieh M., Cosgrove D.J.;
 RT "Molecular cloning and sequence analysis of expansin--a highly
 RT conserved, multigene family of proteins that mediate cell wall
 RT extension in plants.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:9245-9249(1995).
 DR EMBL; U30476; AAB38070.1; -
 DR Mendel; 6669; Arabid; 1201; 6669.
 DR InterPro; IPRO00882; -
 DR Pfam; PF01357; Pollen_allergen; 1.
 DR PRINTS; PRO1225; EXPANSNFAMILY.
 FT NON_TER 1
 SQ SEQUENCE 237 AA; 25155 MW; 0E5A2CB9C2943682 CRC64;

Query Match 64.4%; Score 38; DB 10; Length 237;
 Best Local Similarity 62.5%; Pred. No. 82;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 KTWGQYQW 8
 : ||| ||
 Db 186 RNMWGQNMQ 193

RESULT 27
 Q92P31 PRELIMINARY; PRT; 239 AA.
 AC Q92P31;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE EXPANSIN PRECURSOR.
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae I;
 OC Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4081;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. 91347; TISSUE=FRUIT;

RX MEDLINE=99178803; PubMed=10080718;
 RA Brumwell D.A., Harpster M.H., Dunsmlir P.,
 RT "Differential expression of expansin gene family members during growth
 and ripening of tomato fruit."
 RL Plant Mol. Biol. 39:161-169(1999).
 DR EMBL: AF059489; AAD13633.1; -
 DR Medel: 36058; Lycex:1201;36058.
 DR InterPro: IPR000882; -
 DR Pfam: PF01357; Pollen_allergen; 1.
 DR PRINTS: PR01225; EXPANSNFAMILY.
 DR PRODOM: PD002179; -; 1.
 KW Signal.
 FT CHAIN 1 20 POTENTIAL.
 FT SIGNAL 21 239 * EXPANSIN.
 SQ SEQUENCE 239 AA; 25606 MW; 1C43BF3A1021788C CRC64;

Query Match 64.4%; Score 38; DB 10; Length 239;
 Best Local Similarity 62.5%; Pred. No. 83;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 KTWGQYWQ 8
 : ||| ||
 Db 188 RNMGONMQ 195

RESULT 28

O9LIB1 PRELIMINARY; PRT; 242 AA.
 AC O9LIB1;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE EXPANSIN 3.
 OS Zinnia elegans.
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 CC Magnoliophyta; eudicotyledons; core eudicots; Asteridae;
 CC eusterids II; Asterales; Asteraceae; Heliantheae;
 OC Zinnia.
 OX NCBI_TaxID=34245;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20317189; PubMed=10859177;
 RA Im K.H., Cosgrove D.J., Jones A.M.,
 RT "Subcellular localization of expansin mRNA in xylem cells."
 RL Plant Physiol. 123:463-470(2000).
 DR EMBL: AF230333; AAF35902.1; -
 DR InterPro: IPR000882; -
 DR Pfam: PF01357; Pollen_allergen; 1.
 DR PRINTS: PR01225; EXPANSNFAMILY.
 DR PRODOM: PD002179; -; 1.
 SQ SEQUENCE 242 AA; 26157 MW; 168A01724FCF5B58 CRC64;

Query Match 64.4%; Score 38; DB 10; Length 242;
 Best Local Similarity 62.5%; Pred. No. 84;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 KTWGQYWQ 8
 : ||| ||
 Db 191 RNMGONMQ 198

RESULT 29

O9LIB2 PRELIMINARY; PRT; 245 AA.
 AC O9LIB2;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE EXPANSIN 2.
 OS Zinnia elegans.
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae;
 CC eusterids II; Asterales; Asteraceae; Heliantheae;
 OC Zinnia.
 OX NCBI_TaxID=34245;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20317189; PubMed=10859177;
 RA Im K.H., Cosgrove D.J., Jones A.M.,
 RT "Subcellular localization of expansin mRNA in xylem cells."
 RL Plant Physiol. 123:463-470(2000).
 DR EMBL: AF230332; AAF35901.1; -
 DR InterPro: IPR000882; -
 DR Pfam: PF01357; Pollen_allergen; 1.
 DR PRINTS: PR01225; EXPANSNFAMILY.
 DR PRODOM: PD002179; -; 1.
 SQ SEQUENCE 245 AA; 26201 MW; F6E26114C27E360 CRC64;

Query Match 64.4%; Score 38; DB 10; Length 245;
 Best Local Similarity 62.5%; Pred. No. 85;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 KTWGQYWQ 8
 : ||| ||
 Db 195 RNMGONMQ 202

RESULT 30

O9FNT1 PRELIMINARY; PRT; 245 AA.
 ID O9FNT1;
 AC O9FNT1;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE EXPANSIN.
 OS Cicer arietinum (Chickpea) (Garbanzo).
 CC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 CC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
 CC Fabales; Fabaceae; Papilionoideae; Cicer.
 OX NCBI_TaxID=3827;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. CASTELLANA; TISSUE=ETIOLATED EPICOTYLS;
 RA Dopico B., Sanchez M.A., Labrador E.,
 RT "An expansin is expressed in chickpea epicotyls."
 RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AJ291816; CAC19183.1; -
 SQ SEQUENCE 245 AA; 26469 MW; 0EF6BFC85A38B23 CRC64;

Query Match 64.4%; Score 38; DB 10; Length 245;
 Best Local Similarity 62.5%; Pred. No. 85;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 KTWGQYWQ 8
 : ||| ||
 Db 193 RNMGONMQ 200

Search completed: July 3, 2001, 10:28:11
 Job time: 331 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw Model

Run on: July 3, 2001, 10:28:37 ; Search time 14.6 Seconds
(without alignments)
21.116 Million cell updates/sec

Title: US-09-214-836-9
Perfect score: 59
Sequence: 1 KTWGQYMOV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues
Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	661	1 PM17_HUMAN	P40967 homo sapien
2	55	93.2	626	1 PM17_MOUSE	O60696 mus musculu
3	50	84.7	762	1 P115_CHICK	O98917 gallus gall
4	45	76.3	335	1 PTPI_YEAST	P25044 saccharomyc
5	45	76.3	549	1 YFAQ_ECOLI	P76463 escherichia
6	41	69.5	277	1 CYST_ECOLI	P16701 escherichia
7	41	69.5	315	1 CCSA_CHLUV	P56315 chlorella v
8	41	69.5	328	1 CCSA_ARATH	P56770 arabidopsis
9	41	69.5	340	1 APBE_BUCAP	O85292 buchnera ap
10	40	67.8	515	1 COAT_TRSV	O88894 tobacco rin
11	40	67.8	807	1 YCDS_ECOLI	P75907 escherichia
12	39	66.1	208	1 FCP_ISOGA	O39709 isochrysis
13	39	66.1	794	1 YB52_MYCPN	P75034 mycoplasma
14	38	64.4	100	1 POL_SIV3	P12501 simian immu
15	38	64.4	585	1 PT2B_ARATH	P46032 arabidopsis
16	38	64.4	586	1 YEIH_ECOLI	P33919 escherichia
17	38	64.4	1009	1 YE88_METJA	O58863 methanococc
18	38	64.4	1046	1 POL_SIV4	P27980 simian immu
19	38	64.4	1047	1 POL_SIV1	P27973 simian immu
20	38	64.4	1057	1 POL_SIV1	O02836 simian immu
21	38	64.4	1061	1 POL_SIV1	P05895 simian immu
22	37	62.7	280	1 UBIA_ECOLI	P26601 escherichia
23	37	62.7	305	1 SLEB_ECOLI	P50739 bacillus su
24	37	62.7	394	1 LIP3_DROME	O46108 drosophila
25	37	62.7	623	1 YFE9_YEAST	P43554 saccharomyc
26	37	62.7	677	1 YD64_MYCPN	P75417 mycoplasma
27	37	62.7	1034	1 POL_HV2CA	P24107 human immu
28	37	62.7	1035	1 POL_HV2CA	O74120 human immu
29	37	62.7	1035	1 POL_HV2WZ	P05962 human immu
30	37	62.7	1035	1 POL_HV2SB	P12451 human immu
31	37	62.7	1036	1 POL_HV2RO	P04584 human immu
32	37	62.7	1049	1 POL_HV2G1	P18042 human immu
33	37	62.7	1055	1 POL_HV2ST	P20876 human immu

34	37	62.7	1073	1 POL_HV2D1	P17577 human immu
35	37	62.7	1142	1 POL_HV2BE	P18066 human immu
36	37	62.7	2211	1 FA5_BOVIN	Q28107 bos taurus
37	37	62.7	2224	1 FA5_HUMAN	P12259 homo sapien
38	36	61.0	120	1 PA21_BUNMU	P00617 bungarus mu
39	36	61.0	120	1 PA23_BUNMU	P00619 bungarus mu
40	36	61.0	145	1 PA22_BUNMU	P00618 bungarus mu
41	36	61.0	147	1 PA24_BUNMU	P17934 bungarus mu
42	36	61.0	240	1 XYNC_STRLI	P26220 streptomyces
43	36	61.0	251	1 VG37_BPM1	P08231 bacterioph
44	36	61.0	251	1 VG37_BPOX2	P08232 bacterioph
45	36	61.0	262	1 PAAG_ECOLI	P77467 escherichia

ALIGNMENTS

RESULT 1
ID PM17_HUMAN STANDARD; PRT; 661 AA.
AC P40967; Q16565; Q14817; Q12763; Q14448;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE MELANOCYTE PROTEIN PMEL 17 PRECURSOR (MELANOCYTE LINEAGE-SPECIFIC
ANTIGEN GP100) (MELANOMA-ASSOCIATED ME20 ANTIGEN) (ME20/ME20S)
DE (ME20-M/ME20-S) (95 KDA MELANOCYTE-SPECIFIC SECRETED GLYCOPROTEIN).
GN SLIV OR PMEL17 OR D12S53E.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_Taxid=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92021023; PubMed=1924386;
RA Kwon B.S., Chittamaneni C., Kozak C.A., Copeland N.G.,
RA Gilbert D.J., Jenkins N.A., Barton D., Francke U., Kobayashi Y.,
RA Kim K.-K.;
RT "A melanocyte-specific gene, Pmel 17, maps near the silver coat color
RT locus on mouse chromosome 10 and is in a syntenic region on human
RT chromosome 12.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:9228-9232(1991).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94327566; PubMed=7519602;
RA Adema G.J., de Boer A.J., Vogel A.M., Loenen W.A., Figdor C.G.;
RT "Molecular characterization of the melanocyte lineage-specific
RT antigen gp100.";
RL J. Biol. Chem. 269:20126-20133(1994).
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96154052; PubMed=8592076;
RA Ballin T., Lee S.T., Spritz R.A.;
RT "Genomic organization and sequence of D12S53E (Pmel 17), the human
RT homologue of the mouse silver (si) locus.";
RL J. Invest. Dermatol. 106:24-27(1996).
[4]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 25-53.
RX MEDLINE=94235165; PubMed=8179825;
RA Marsh G.A., Marken J.S., Neubauer M., Aruffo A., Hellstrom I.,
RA Hellstrom K.E., Marguardt H.;
RT "Cloning and expression of the gene for the melanoma-associated ME20
RT antigen.";
RL DNA Cell Biol. 13:87-95(1994).
[5]
RP SEQUENCE FROM N.A.
RX Kwon B.S., Kim K., Heng H.H., Shi X.M., Tsui L., Lee Z.H.,
RA Yoon B., Pickard R.T.;
RT Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
[6]
RP SEQUENCE FROM N.A.
RX Vogel A.;
RT Submitted (NOV-1990) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: COULD BE A MELANOGENIC ENZYME. COULD REPRESENT AN
 CC ONCOFETAL SELF-ANTIGEN THAT IS NORMALLY EXPRESSED AT LOW LEVELS IN
 CC QUIESCENT ADULT MELANOCYTES BUT OVEREXPRESSED BY PROLIFERATING
 CC NEONATAL MELANOCYTES AND DURING TUMOR GROWTH. RELEASE OF THE
 CC SOLUBLE FORM, ME20-S, COULD PROTECT TUMOR CELLS FROM ANTIBODY
 CC MEDIATED IMMUNITY.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL). THERE
 CC IS ALSO A SECRETED SOLUBLE FORM, ME20-S, PROBABLY PRODUCT OF
 CC PROTEOLYTIC CLEAVAGE.
 CC -1- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN MELANOMAS. SOME
 CC EXPRESSION WAS FOUND IN DYSPLASTIC NEVI. NOT FOUND IN NORMAL
 CC TISSUES NOR IN CARCINOMAS.
 CC -1- SIMILARITY: BELONGS TO THE PMEL-17/NNB FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 PKD DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M77348; AAA60121.1; -
 DR EMBL: S73003; AAC00634.1; -
 DR EMBL: U31799; AAB00386.1; -
 DR EMBL: U31808; AAB00386.1; JOINED.
 DR EMBL: U31807; AAB00386.1; JOINED.
 DR EMBL: U31797; AAB00386.1; JOINED.
 DR EMBL: U31798; AAB00386.1; JOINED.
 DR EMBL: U01874; AAB18479.1; -
 DR EMBL: U20093; AAB19181.1; -
 DR EMBL: U19491; AAB19181.1; JOINED.
 DR EMBL: M32295; AAA35930.1; ALT_INIT.
 DR MIM: 155550; -
 DR Interpro: IPR000601; -
 DR Pfam: PF00801; PKD; 1.
 DR PROSITE: PS50093; PKD; 1.
 DR Transmembrane: Glycoprotein; signal; Melanin biosynthesis; Repeat;
 KW Antigen.
 FT SIGNAL. 1 24
 FT CHAIN 25 661
 FT DOMAIN 25 595
 FT TRANSMEM 596 616
 FT DOMAIN 617 661
 FT DOMAIN 255 292
 FT DOMAIN 315 444
 FT REPEAT 315 327
 FT REPEAT 328 340
 FT REPEAT 341 353
 FT REPEAT 354 366
 FT REPEAT 367 379
 FT REPEAT 380 392
 FT REPEAT 393 405
 FT REPEAT 406 418
 FT REPEAT 419 431
 FT REPEAT 432 444
 FT CARBOHYD 81 106
 FT CARBOHYD 106 111
 FT CARBOHYD 111 111
 FT CARBOHYD 321 321
 FT CARBOHYD 568 568
 FT CARBOHYD 274 274
 FT CONFLICT 587 587
 FT CONFLICT 592 592
 FT CONFLICT 597 597
 FT CONFLICT 642 661
 FT SEQUENCE 661 AA; 70255 MW; 8A904FAB16715653 CRC64;
 SQ

Query Match 100.0%; Score 59; DB 1; Length 661;
 Best Local Similarity 100.0%; Pred. NO. 0.035;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 KTMGOTWYV 9
 Db 154 KTMGOTWYV 162
 RESULT 2
 ID PM17_MOUSE
 AC 060696; STANDARD; PRT; 626 AA.
 DT 01-NOV-1997 (Rel. 35, Created).
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE MELANOCYTE PROTEIN PMEL 17 PRECURSOR (SILVER LOCUS PROTEIN).
 GN SILV OR PMEL17 OR D10H12S53E OR SI.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Skin;
 RX MEDLINE=95175358; PubMed=7870580;
 RA Kwon B.-S., Halaban R., Ponnazhagan S., Kim K., Chintamaneni C.,
 RA Bennett D., Pickard R.T.;
 RT "Mouse silver mutation is caused by a single base insertion in the
 RT putative cytoplasmic domain of pmel 17."
 RL Nucleic Acids Res. 23:154-158(1995).
 CC -1- FUNCTION: COULD BE A MELANOGENIC ENZYME.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN MELANOCYTES.
 CC -1- DISEASE: DEFECTS IN PMEL17 ARE THE CAUSE OF THE SILVER COAT COLOR
 CC WHICH SEEMS TO BE DUE TO PREMATURE DEATH OF PIGMENT CELLS DURING
 CC THE HAIR CYCLE.
 CC -1- SIMILARITY: BELONGS TO THE PMEL-17/NNB FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 PKD DOMAIN.
 CC -----
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 CC -----
 DR EMBL: U14133; AAA69538.1; -
 DR MGD: MGI:98301; SI.
 DR PROSITE: PS50093; PKD; 1.
 DR Transmembrane: Glycoprotein; signal; Melanin biosynthesis; Repeat;
 KW Disease mutation.
 FT SIGNAL. 1 24
 FT CHAIN 25 626
 FT DOMAIN 25 562
 FT TRANSMEM 563 583
 FT DOMAIN 584 626
 FT DOMAIN 255 292
 FT DOMAIN 315 411
 FT REPEAT 315 327
 FT REPEAT 328 340
 FT REPEAT 341 353
 FT REPEAT 354 366
 FT REPEAT 367 379
 FT REPEAT 380 392
 FT REPEAT 393 411
 FT CARBOHYD 81 81
 FT CARBOHYD 106 106
 FT CARBOHYD 111 111
 FT CARBOHYD 535 535
 FT CARBOHYD 170 170
 FT VARIANT 175 175
 FT VARIANT 175 175
 FT VARIANT 471 471
 FT VARIANT 471 471
 FT SEQUENCE 471 AA; 50255 MW; 8A904FAB16715653 CRC64;
 SQ

FT VARIANT 603 626 AAPASGLARGLGENSPILSGOV -> SSASIRSSRRPM
 FT SEQUENCE 626 AA: 65980 MW: 7AB941D2B3FB1044 CRC64:
 SQ

Query Match
 Best Local Similarity 93.2%; Score 55; DB 1; Length 626;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KTWGQYOV 9
 1111111111
 DB 154 KTWGKRYOV 162

RESULT 3
 P115_CHICK STANDARD; PRT; 762 AA.
 AC 098917;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE MELANOSOMAL MATRIX PROTEIN 115 KDA PROTEIN PRECURSOR.
 GN MPM115.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WHITE LEGHORN; TISSUE=retinal pigment epithelium;
 RX MEDLINE=92020667; PubMed=1924173;
 RA Mochizuki M., Agata K., Eguchi G.;
 RT "Complete sequence and expression of a cDNA encoding a chicken
 RT 115-kDa melanosomal matrix protein."
 RT Pigment Cell Res. 4:41-47(1991).
 RL [2]
 RN CHARACTERIZATION.
 RP STRAIN=WHITE LEGHORN; TISSUE=retinal pigment epithelium;
 RX MEDLINE=88311098; PubMed=3409326;
 RA Mochizuki M., Agata K., Kobayashi H., Yamamoto T.S., Eguchi G.;
 RT "Expression of gene coding for a melanosomal matrix protein
 RT transcriptionally regulated in the transdifferentiation of chick
 RT embryo pigmented epithelial cells."
 RL Cell Differ. 24:67-74(1988).
 CC -1- FUNCTION: MIGHT BE REQUIRED FOR POLYMERIZATION OF MELANIN ONTO THE
 CC CORE STRUCTURE OF MELANOSOMES WITH ENZYMIC FUNCTION OF TYROSINASE.
 CC -1- SUBCELLULAR LOCATION: ON THE FIBROUS MATRIX STRUCTURE OF THE
 CC PREMELANOSOME.
 CC -1- TISSUE SPECIFICITY: SPECIFIC TO PIGMENTED EPITHELIAL CELLS AND
 CC MELANOCYTES. NOT EXPRESSED IN LENS, NEURAL RETINA, BRAIN, HEART,
 CC GIZZARD OR LIVER.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING THE REDIFFERENTIATION OF
 CC PIGMENTED EPITHELIAL CELLS (PEC).
 CC -1- PTM: GLYCOSYLATED.
 CC -1- SIMILARITY: BELONGS TO THE PHEM-17/NMB FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 PKD DOMAIN.
 CC -----
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 CC -----
 CC EMBL: D88348; BAA13589.1; -
 CC InterPro: IPR000601; -
 CC Pfam: PF00801; PKD.1.
 CC PROSITE: PS50093; PKD.1.
 CC Signal: Glycoprotein; Repeat.
 CC SIGNAL 1 19 POTENTIAL.
 CC CHAIN 20 762 MELANOSOMAL MATRIX PROTEIN 115 KDA

FT DOMAIN 223 323 PROTEIN.
 FT DOMAIN 441 532 PKD. 4 X 20-24 AA APPROXIMATE TANDEM REPEATS.
 FT REPEAT 441 464 1.
 FT REPEAT 465 488 2.
 FT REPEAT 489 508 3.
 FT REPEAT 509 532 4.
 FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 346 346 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 651 651 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 659 659 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 762 AA: 77356 MW: 172C8DB4FDC67C6 CRC64:

Query Match
 Best Local Similarity 84.7%; Score 50; DB 1; Length 762;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 TWGQYOV 9
 1111111111
 DB 161 TWGKRYOV 168

RESULT 4
 PTP1_YEAST STANDARD; PRT; 335 AA.
 AC P25044;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE PROTEIN-TYROSINE PHOSPHATASE 1 (EC 3.1.3.48) (PTPASE 1).
 GN PTP1 OR YDL230W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91302312; PubMed=1649172;
 RA Guan K., Deschenes R.J., Qiu H., Dixon J.E.;
 RT "Cloning and expression of a yeast protein tyrosine phosphatase."
 RT J. Biol. Chem. 266:12964-12970(1991).
 RL [2]
 RN
 RP
 CC SEQUENCE FROM N.A.
 CC Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: IS NOT REQUIRED FOR VEGETATIVE GROWTH.
 CC -1- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O =
 CC PROTEIN TYROSINE + ORTHOPHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 CC TYROSINE PHOSPHATASE FAMILY.
 CC -----
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 CC -----
 CC EMBL: M64062; AAA34923.1; -
 CC EMBL: Z74278; CAA98809.1; -
 CC PIR: A39862; A39862.
 CC HSP: P18052; 1YPO.
 CC SGD: S0002389; PTP1.
 CC InterPro: IPR000242; -
 CC InterPro: IPR000387; -
 CC Pfam: PF00102; 1-Phosphatase; 1.
 CC PRINTS: PR00700; PTPPHPTASE.
 CC PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
 CC PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.

DR	PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
KW	Hydrolase.
FT	252 BY SIMILARITY.
ACT_SITE	38868 MM; 15F71E50694B5E62
SEQUENCE	335 AA; CRC64

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CC -----
DR EMBL; AE000312; AAC75286.1; -;
DR Ecogene; EGI4079; yfaQ.
KW Hypothetical protein; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 549 HYPOTHETICAL PROTEIN YFAQ.
SQ SEQUENCE 549 AA; 61475 MW; 72C26716D953C9D1 CRC64;

CN	CYSU OR CYST.
OS	Escherichia coli.
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC	Escherichia.
OX	NCBI_TaxID=562;
RA	[1]
RA	SEQUENCE FROM N.A.
RC	STRAIN-K12:
RC	MEDLINE=90264334; PubMed=2188958;
RC	Sitko A., Hyrniiewicz M.M., Hulanicka D.M., Boeck A.,
RA	"Sulfite and thiosulfate transport in Escherichia coli K-12:
RA	nucleotide sequence and expression of the cystSWAM gene cluster."
RA	J. Bacteriol. 172:3351-3357(1990).
RA	[2]
RA	SEQUENCE FROM N.A.
RA	STRAIN-K12 / MG1655;
RA	MEDLINE=97426617; PubMed=9278503;
RA	Blather F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA	Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA	Gregor J., Davis N.W., Kirpatrick H.A., Goeden M.A., Rose D.J.,
RA	Mau B., Shao Y.;
RA	"The complete genome sequence of Escherichia coli K-12."
RA	science 277:1453-1474(1997).
RA	[3]
RA	SEQUENCE FROM N.A.
RA	STRAIN-K12;
RA	MEDLINE=97349980; PubMed=9205837;
RA	Yanamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K.,
RA	Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
RA	Mitsubuchi K., Mori H., Nakade S., Nakamura Y., Nishimoto H.,
RA	Osima T., Oyama T., Saito N., Sempel G., Satoh Y., Sivasubaram S.,
RA	Tagami H., Takahashi T., Takeda J., Takemoto K., Uehara K., Wada C.,
RA	Yanagata S., Horiiuchi T.;
RA	"Construction of a contiguous 874-kb sequence of the Escherichia coli
RA	K-12 genome corresponding to 50.0-68.8 min on the linkage map and
RA	analysis of its sequence features."
RA	DNA Res. 4:91-113(1997).
RA	-1- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
RA	FOR SULFATE AND THIOSULFATE. PROBABLY RESPONSIBLE FOR THE
RA	TRANSLLOCATION OF THE SUBSTRATE ACROSS THE MEMBRANE.
RA	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
RA	(POTENTIAL).
RA	-1- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
RA	PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE CYSTM
RA	SUBFAMILY.
RA	-----
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RA	-----
RA	EMBL; M32101; AAA23637.1; -
RA	EMBL; AE000330; AAC75477.1; -
RA	EMBL; D90871; BAA16298.1; -
RA	EMBL; D90872; BAA16307.1; -
RA	PIR; A35402; QRECSY.
RA	PIR; B35403; B35403.
RA	Ecogene; EG10197; cystU.
RA	InterPro; IPR000515; -
RA	Pfam; PF00528; BPD_transp.1.
RA	PROSITE; PS00402; BPD_TRANSP_INN_MEMBER.1.
RA	Inner membrane; Transmembrane; Sulfate transport; Transport.
RA	FT TRANSMEM 21 39 POTENTIAL.
RA	FT TRANSMEM 64 80 POTENTIAL.
RA	FT TRANSMEM 105 121 POTENTIAL.
RA	FT TRANSMEM 140 156 POTENTIAL.
RA	FT TRANSMEM 188 204 POTENTIAL.
RA	FT TRANSMEM 247 259 POTENTIAL.
RA	SEQUENCE 277 AA; 30291 MW; 1392821BDDE24459 CRC64;

Query Match 69.5%; Score 41; DB 1; Length 277;
 Best Local Similarity 62.5%; Pred. No. 9.1;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 TWGQYV 9
 :|||:
 Db 43 SNAQYWEV 50

RESULT 7
 CCSA_CHLVU STANDARD; PRT; 315 AA.
 ID P56315;
 AC 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE CYTOCHROME C BIOGENESIS PROTEIN CCSA.
 GN Chlorocella vulgaris.
 OS Chloroplast.
 OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
 CC Chlorellaceae; Chlorocella.
 RX NCBI_TaxID=3077;
 RP SEQUENCE FROM N.A.
 RC STRAIN=IAM C-27 / TAMITA;
 RA MEDLINE=97303241; PubMed=9159184;
 RA Nakasugi T., Nagai T., Kapoor M., Sugita M., Ito M., Ito S.,
 RA Tsudzuki J., Nakashima K., Tsudzuki T., Suzuki Y., Hamada A., Ohta T.,
 RA Imanura A., Yoshinaga K., Sugitara M.;
 RT "Complete nucleotide sequence of the chloroplast genome from the
 RT green alga Chlorocella vulgaris: the existence of genes possibly
 RT involved in chloroplast division."
 RL Proc. Natl. Acad. Sci. U.S.A. 94:5967-5972(1997).
 CC -1- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
 CC HEME ATTACHMENT (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL/NRFE/CCSA FAMILY.
 CC -----
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 CC -----
 CC DR EMBL; AB001684; BAA57962.1;
 DR InterPro; IPR002541;
 DR Pfam; PF01578; Cytc.asm; 1.
 KW Cytochrome c-type biogenesis; Chloroplast.
 SQ SEQUENCE 315 AA; 35471 MW; 5020388E94FE4F10 CRC64;

Query Match 69.5%; Score 41; DB 1; Length 315;
 Best Local Similarity 71.4%; Pred. No. 10;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYV 7
 :|||:
 Db 243 ETWGNW 249

RESULT 8
 CCSA_ARATH STANDARD; PRT; 328 AA.
 ID P56770;
 AC 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE CYTOCHROME C BIOGENESIS PROTEIN CCSA.
 GN CCSA.
 OS Arabidopsis thaliana (Mouse-ear cress).

OG Chloroplast.
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Eudicotyledons; core eudicots; rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=20039611; PubMed=10574454;
 RA Sato S., Nakamura Y., Kaneko T., Asamizu E., Tabata S.;
 RT "Complete structure of the chloroplast genome of Arabidopsis
 RT thaliana."
 RL DNA Res. 6:283-290(1999).
 CC -1- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
 CC HEME ATTACHMENT (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL/NRFE/CCSA FAMILY.
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 CC -----
 CC DR EMBL; AP000423; BAA84436.1;
 DR InterPro; IPR002541;
 DR Pfam; PF01578; Cytc.asm; 1.
 KW Cytochrome c-type biogenesis; Chloroplast.
 SQ SEQUENCE 328 AA; 37732 MW; C8BD1508B2924D6F CRC64;

Query Match 69.5%; Score 41; DB 1; Length 328;
 Best Local Similarity 71.4%; Pred. No. 11;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYV 7
 :|||:
 Db 255 ETWGSYV 261

RESULT 9
 APBE_BUCAP STANDARD; PRT; 340 AA.
 ID O85292;
 AC 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE PROBABLE THIAMINE BIOSYNTHESIS PROTEIN APBE PRECURSOR.
 GN APBE.
 OS Buchnera aphidicola (subsp. Schizaphis graminum).
 CC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
 OX NCBI_TaxID=98794;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98353428; PubMed=9688822;
 RA Thao M.L., Baumann P.;
 RT "Sequence analysis of a DNA fragment from Buchnera aphidicola (Aphid
 RT endosymbiont) containing the genes dapD-htra-llvH-ftsL-ftsI-
 RT mure."
 RL Curr. Microbiol. 37:214-216(1998).
 RN [2]
 RP REVISIONS.
 RA Thao M.L., Baumann P.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INVOLVED IN THE CONVERSION OF AMINOIMIDAZOLE RIBOTIDE
 CC (AIR), A PURINE INTERMEDIATE, TO THE 4-AMINO-5-HYDROXYMETHYL-2-
 CC METHYL PYRIMIDINE (HMP) MOIETY OF THIAMINE (BY SIMILARITY).
 CC -1- PATHWAY: BIOSYNTHESIS OF THE PYRIMIDINE MOIETY OF THIAMINE.
 CC -1- SIMILARITY: BELONGS TO THE APBE FAMILY.
 CC -----
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DR EMBL: AF060492; AAC32332.2; -

KW Thiamine biosynthesis; Signal.

FT SIGNAL 1 340 POTENTIAL.

FT CHAIN ? 340 PROBABLE THIAMINE BIOSYNTHESIS PROTEIN

FT ABBE.

SEQUENCE 340 AA; 38703 MW; 70EBABCCF8754C5C CRC64;

Query Match 69.5%; Score 41; DB 1; Length 340;

Best Local Similarity 77.8%; Pred. No. 11;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTWGYWQV 9

DB 34 KTWGYWQV 42

RESULT 10

COAT_TRSV STANDARD; PRT; 515 AA.

AC 088894;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE COAT PROTEIN PRECURSOR (CAPSID PROTEIN).

OS Tobacco ringspot virus (Tobsv) (TRSV).

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;

OC Nepovirus.

OX NCBI_TaxID=12282;

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RX MEDLINE-94152161; PubMed-8109164;

RA Buckley B., Silva S., Singh S.;

RT "Nucleotide sequence and in vitro expression of the capsid protein

gene of tobacco ringspot virus.";

RL Virus Res. 30:335-349(1993).

RN [2]

RP ERATUM.

RX MEDLINE-95274284; PubMed-7754671;

RA Buckley B., Silva S., Singh S.;

RL Virus Res. 35:111-111(1995).

RN [3]

RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).

RX MEDLINE-98179933; PubMed-9519407;

RA Chandrasekar V., Johnson J.E.;

RT "The structure of tobacco ringspot virus: a link in the evolution of

icosahedral capsids in the picornavirus superfamily.";

RL Structure 6:157-171(1998).

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RX MEDLINE-94152161; PubMed-8109164;

RA Buckley B., Silva S., Singh S.;

RT "Nucleotide sequence and in vitro expression of the capsid protein

gene of tobacco ringspot virus.";

RL Virus Res. 30:335-349(1993).

RN [2]

RP ERATUM.

RX MEDLINE-95274284; PubMed-7754671;

RA Buckley B., Silva S., Singh S.;

RL Virus Res. 35:111-111(1995).

RN [3]

RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).

RX MEDLINE-98179933; PubMed-9519407;

RA Chandrasekar V., Johnson J.E.;

RT "The structure of tobacco ringspot virus: a link in the evolution of

icosahedral capsids in the picornavirus superfamily.";

RL Structure 6:157-171(1998).

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RX MEDLINE-94152161; PubMed-8109164;

RA Buckley B., Silva S., Singh S.;

RT "Nucleotide sequence and in vitro expression of the capsid protein

gene of tobacco ringspot virus.";

RL Virus Res. 30:335-349(1993).

RN [2]

RP ERATUM.

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RA Buckley B., Silva S., Singh S.;

RL Virus Res. 35:111-111(1995).

RN [3]

RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).

RX MEDLINE-98179933; PubMed-9519407;

RA Chandrasekar V., Johnson J.E.;

RT "The structure of tobacco ringspot virus: a link in the evolution of

icosahedral capsids in the picornavirus superfamily.";

RL Structure 6:157-171(1998).

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RX MEDLINE-94152161; PubMed-8109164;

RA Buckley B., Silva S., Singh S.;

RT "Nucleotide sequence and in vitro expression of the capsid protein

gene of tobacco ringspot virus.";

RL Virus Res. 30:335-349(1993).

RN [2]

RP ERATUM.

RX MEDLINE-95274284; PubMed-7754671;

RA Buckley B., Silva S., Singh S.;

RL Virus Res. 35:111-111(1995).

RN [3]

RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).

RX MEDLINE-98179933; PubMed-9519407;

RA Chandrasekar V., Johnson J.E.;

RT "The structure of tobacco ringspot virus: a link in the evolution of

icosahedral capsids in the picornavirus superfamily.";

RL Structure 6:157-171(1998).

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RX MEDLINE-94152161; PubMed-8109164;

RA Buckley B., Silva S., Singh S.;

RT "Nucleotide sequence and in vitro expression of the capsid protein

gene of tobacco ringspot virus.";

RL Virus Res. 30:335-349(1993).

RN [2]

RP ERATUM.

RX MEDLINE-95274284; PubMed-7754671;

RA Buckley B., Silva S., Singh S.;

RL Virus Res. 35:111-111(1995).

RN [3]

RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).

RX MEDLINE-98179933; PubMed-9519407;

RA Chandrasekar V., Johnson J.E.;

RT "The structure of tobacco ringspot virus: a link in the evolution of

icosahedral capsids in the picornavirus superfamily.";

RL Structure 6:157-171(1998).

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RX MEDLINE-94152161; PubMed-8109164;

RA Buckley B., Silva S., Singh S.;

RT "Nucleotide sequence and in vitro expression of the capsid protein

gene of tobacco ringspot virus.";

RL Virus Res. 30:335-349(1993).

RN [2]

RP ERATUM.

RX MEDLINE-95274284; PubMed-7754671;

RA Buckley B., Silva S., Singh S.;

RL Virus Res. 35:111-111(1995).

RN [3]

RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).

RX MEDLINE-98179933; PubMed-9519407;

RA Chandrasekar V., Johnson J.E.;

RT "The structure of tobacco ringspot virus: a link in the evolution of

icosahedral capsids in the picornavirus superfamily.";

RL Structure 6:157-171(1998).

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RX MEDLINE-94152161; PubMed-8109164;

RA Buckley B., Silva S., Singh S.;

RT "Nucleotide sequence and in vitro expression of the capsid protein

gene of tobacco ringspot virus.";

RL Virus Res. 30:335-349(1993).

RN [2]

RP ERATUM.

RX MEDLINE-95274284; PubMed-7754671;

RA Buckley B., Silva S., Singh S.;

RL Virus Res. 35:111-111(1995).

RN [3]

RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).

RX MEDLINE-98179933; PubMed-9519407;

RA Chandrasekar V., Johnson J.E.;

RT "The structure of tobacco ringspot virus: a link in the evolution of

icosahedral capsids in the picornavirus superfamily.";

RL Structure 6:157-171(1998).

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RX MEDLINE-94152161; PubMed-8109164;

RA Buckley B., Silva S., Singh S.;

RT "Nucleotide sequence and in vitro expression of the capsid protein

gene of tobacco ringspot virus.";

RL Virus Res. 30:335-349(1993).

RN [2]

RP ERATUM.

RX MEDLINE-95274284; PubMed-7754671;

RA Buckley B., Silva S., Singh S.;

RL Virus Res. 35:111-111(1995).

RN [3]

RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).

RX MEDLINE-98179933; PubMed-9519407;

RA Chandrasekar V., Johnson J.E.;

RT "The structure of tobacco ringspot virus: a link in the evolution of

icosahedral capsids in the picornavirus superfamily.";

RL Structure 6:157-171(1998).

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RX MEDLINE-94152161; PubMed-8109164;

RA Buckley B., Silva S., Singh S.;

RT "Nucleotide sequence and in vitro expression of the capsid protein

gene of tobacco ringspot virus.";

RL Virus Res. 30:335-349(1993).

RN [2]

RP ERATUM.

RX MEDLINE-95274284; PubMed-7754671;

RA Buckley B., Silva S., Singh S.;

RL Virus Res. 35:111-111(1995).

RN [3]

RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).

RX MEDLINE-98179933; PubMed-9519407;

RA Chandrasekar V., Johnson J.E.;

RT "The structure of tobacco ringspot virus: a link in the evolution of

icosahedral capsids in the picornavirus superfamily.";

RL Structure 6:157-171(1998).

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RX MEDLINE-94152161; PubMed-8109164;

RA Buckley B., Silva S., Singh S.;

RT "Nucleotide sequence and in vitro expression of the capsid protein

gene of tobacco ringspot virus.";

RL Virus Res. 30:335-349(1993).

RN [2]

RP ERATUM.

RX MEDLINE-95274284; PubMed-7754671;

RA Buckley B., Silva S., Singh S.;

RL Virus Res. 35:111-111(1995).

RN [3]

RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).

RX MEDLINE-98179933; PubMed-9519407;

RA Chandrasekar V., Johnson J.E.;

RT "The structure of tobacco ringspot virus: a link in the evolution of

icosahedral capsids in the picornavirus superfamily.";

RL Structure 6:157-171(1998).

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RX MEDLINE-94152161; PubMed-8109164;

RA Buckley B., Silva S., Singh S.;

RT "Nucleotide sequence and in vitro expression of the capsid protein

gene of tobacco ringspot virus.";

RL Virus Res. 30:335-349(1993).

RN [2]

RP ERATUM.

RX MEDLINE-95274284; PubMed-7754671;

RA Buckley B., Silva S., Singh S.;

RL Virus Res. 35:111-111(1995).

RN [3]

RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).

RX MEDLINE-98179933; PubMed-9519407;

RA Chandrasekar V., Johnson J.E.;

RT "The structure of tobacco ringspot virus: a link in the evolution of

icosahedral capsids in the picornavirus superfamily.";

RL Structure 6:157-171(1998).

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RX MEDLINE-94152161; PubMed-8109164;

RA Buckley B., Silva S., Singh S.;

RT "Nucleotide sequence and in vitro expression of the capsid protein

gene of tobacco ringspot virus.";

RL Virus Res. 30:335-349(1993).

RN [2]

RP ERATUM.

RX MEDLINE-95274284; PubMed-7754671;

RA Buckley B., Silva S., Singh S.;

RL Virus Res. 35:111-111(1995).

RN [3]

RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).

RX MEDLINE-98179933; PubMed-9519407;

RA Chandrasekar V., Johnson J.E.;

RT "The structure of tobacco ringspot virus: a link in the evolution of

icosahedral capsids in the picornavirus superfamily.";

RL Structure 6:157-171(1998).

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RX MEDLINE-94152161; PubMed-8109164;

RA Buckley B., Silva S., Singh S.;

RT "Nucleotide sequence and in vitro expression of the capsid protein

gene of tobacco ringspot virus.";

RL Virus Res. 30:335-349(1993).

RN [2]

RP ERATUM.

Db 314 MGQY 318

RESULT 12
FCP_ISOQA STANDARD: PRT: 208 AA.
AC 039709;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE FUCOXANTHIN-CHLOROPHYLL A-C BINDING PROTEIN, CHLOROPLAST PRECURSOR (FCP).
GN FCP.
OS Isochrysis galbana.
OC Eukaryota: Haptophyceae; Isochrysidales; Isochrysis.
OX NCBI_TaxID=37099;
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RC STRAIN-DUN;
RX MEDLINE=94325461; PubMed=8049362;
RA Laroche J., Henry D., Wyman K., Sukenik A., Falkowski P.;
RT "Cloning and nucleotide sequence of a cDNA encoding a major fucoxanthin-chlorophyll a/c-containing protein from the chrysophyte Isochrysis galbana: implications for evolution of the cab gene family.";
RT Plant Mol. Biol. 25:355-368(1994).
CC -1- FUNCTION: THE LIGHT-HARVESTING COMPLEX (LHC) FUNCTIONS AS A LIGHT RECEPTOR. IT CAPTURES & DELIVERS EXCITATION ENERGY TO PHOTOSYSTEMS WITH WHICH IT IS CLOSELY ASSOCIATED. ENERGY IS TRANSFERRED FROM THE CAROTENOID AND CHL C (OR-B) TO CHL A AND THE PHOTOSYNTHETIC REACTION CENTERS WHERE IT IS USED TO SYNTHESIZE ATP AND REDUCING POWER.
CC -1- SUBUNIT: THE LHC COMPLEX OF CHROMOPHYTIC ALGAE IS COMPOSED OF FUCOXANTHIN, CHLOROPHYLL A AND C BOUND NON-COVALENTLY BY PIGMENTS IN LHC; FUCOXANTHIN: CHLOROPHYLL C: CHLOROPHYLL A IS (0.6-1): (0.1-0.3): (1).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE. FCPs ARE PROBABLY TRANSPORTED ACROSS THE ENDOPLASMIC RETICULUM MEMBRANES THAT SURROUND THE PLASTID VIA A SIGNAL PEPTIDE, FOLLOWED BY TRANSLOCATION ACROSS THE THYLAKOID MEMBRANE VIA A TRANSIT PEPTIDE.
CC -1- INDUCTION: EXPRESSION IS INCREASED 5-FOLD UNDER CONDITIONS OF LOW LIGHT.
CC -1- SIMILARITY: BELONGS TO THE FCP FAMILY OF LIGHT-HARVESTING PROTEINS.
CC -----
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CC -----
DR EMBL: X77333; CAAS4547.1; -
DR InterPro: IPR001344; -
DR Pfam: PF00504; chloro_a-b-bind. 2
KW Light-harvesting polypeptide; Chloroplast; Photosynthesis;
KW Photosystem II; Multigene family; Chlorophyll; Transmembrane;
KW Thylakoid membrane; Transit peptide.
FT TRANSIT 1 31 CHLOROPLAST (PROBABLE).
FT CHAIN 32 208 FUCOXANTHIN-CHLOROPHYLL A-C BINDING PROTEIN.
FT TRANSMEM 102 118 POTENTIAL.
SQ SEQUENCE 208 AA; 22471 MW; 21A36700137A0F1B CRC64;

Query Match 66.1%; Score 39; DB 1; Length 208;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
2 TWGQY 7
|||||

Db 198 TWGTY 203

RESULT 13
YB52_MYCPN STANDARD: PRT: 794 AA.
AC P75034;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE HYPOTHETICAL LIPOPROTEIN MPN152 PRECURSOR (E07_09F794).
GN MPN152 OR MP002.
OS Mycoplasma pneumoniae.
OC Bacteria: Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelreich R., Hilbert H., Plagens H., Pitkl E., Li B.-C., Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae.";
RT Nucleic Acids Res. 24:4420-4449(1996).
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A LIPID ANCHOR (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE MG185 / MG260 FAMILY.
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CC -----
DR EMBL: AE000001; AAB95650.1; -
KW Hypothetical protein; Lipoprotein; Membrane; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 794 HYPOTHETICAL LIPOPROTEIN MPN152.
FT LIPID 23 23 N-ACYL DIGLYCERIDE (POTENTIAL).
SQ SEQUENCE 794 AA; 86871 MW; 0DA72D12807E53BE CRC64;

Query Match 66.1%; Score 39; DB 1; Length 794;
Best Local Similarity 66.7%; Pred. No. 48;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
1 KTWGQY 9
Db 268 KTWGQY 276
|||||

RESULT 14
POL_STVA3 STANDARD: PRT: 100 AA.
AC P12501;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE POL. POLYPROTEIN (CONTAINS: PROTEASE (RETROPEPSIN) (EC 3.4.23.16); DE REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)) (FRAGMENT).
GN POL.
OS Simian immunodeficiency virus (AGM385 isolate) (SIV-AGM).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11729;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89012184; PubMed=3172340;
RA Daniel M.D., Li Y., Naidu Y.M., Durda P.J., Schmidt D.K., Troup C.D., Silva D.P., Mackey J.J., Kestler H.W., Sehgal P.K.,

RA King N.W., Ohta Y., Hayami M., Desrosiers R.C.;
 RT "Simian immunodeficiency virus from African green monkeys."; J. Virol. 62:4123-4128(1988).
 CC -1- MISCELLANEOUS; THIS IS AN AFRICAN GREEN MONKEY ISOLATE.
 CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO KNOWN AS THE RETROPEPSIN FAMILY.
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 CC -----
 DR EMBL: M21311; AAA47583.1; -.
 DR HSSP: P04585; IKLM.
 DR HIV: M21311; POLSAGM38.
 DR MEROPS: A02.003; -.
 DR InterPro: IPR001969; -.
 DR PROSITE: P500141; ASP_PROTEASE; PARTIAL.
 KW AIDS; Polypeptide; Hydrolyase; Aspartyl protease; Endonuclease;
 KW Nuclease; Transferase; RNA-directed DNA polymerase.
 FT NON_TER 1 100
 FT NON_TER 1 100
 SQ SEQUENCE 100 AA; 12023 MW; FQ11C66792D37E3F CRC64;

Query Match 64.4%; Score 38; DB 1; Length 100;
 Best Local Similarity 71.4%; Pred. No. 10;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 WQGYMOV 9
 Db 26 WADYMOV 32

RESULT 15
 PT2B_ARATH STANDARD; PRT; 585 AA.
 ID PT2B_ARATH
 AC P46032;
 DT 01-NOV-1995 (Rel. 32; Last sequence update)
 DT 01-NOV-1995 (Rel. 32; Last annotation update)
 DT 01-OCT-2000 (Rel. 40; Last annotation update)
 GN PEPTIDE TRANSPORTER PTR2-B (HISTIDINE TRANSPORTING PROTEIN).
 DE PTR2-B OR NTRI OR AT2G02040 OR F14H20.11.
 OS Arabidopsis thaliana (Mouse-ear cress).
 CC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 CC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 CC Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_Taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. LANDSBERG-ERECTA;
 RA Song W., Steiner H.-Y., Zhang L., Naider F., Stacey G.,
 RA Becker J.M.;
 RL Submitted (XXX-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. C24;
 RX MEDLINE=94307379; PubMed=8033999;
 RA Frommer W.B., Hummel S., Reutsch D.;
 RT "Cloning of an Arabidopsis histidine transporting protein related to nitrate and peptide transporters."; FEBS Lett. 347:185-189(1994).
 RL [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.C., Ronning C.M., Koo H., Moffat K.S.,
 RA Cronin L.A., Shen W., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,

RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
 RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
 RA Salberg S.L., Fraser C.M., Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana."; Nature 402:761-768(1999).
 RL [1]
 CC -1- FUNCTION: PEPTIDE TRANSPORT. HIGH AFFINITY, LOW CAPACITY TRANSPORTER. CAN ALSO TRANSPORT HISTIDINE.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE PTR2 FAMILY OF TRANSPORTERS.
 CC -----
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 CC -----
 DR EMBL: L39082; AAB00858.1; -.
 DR EMBL: X77503; CAA54634.1; -.
 DR EMBL: AC006532; AAD20096.1; -.
 DR InterPro: IPR00109; -.
 DR Pfam: PF00854; PTR2.1;
 DR PROSITE: PS01022; PTR2_1;
 DR PROSITE: PS01023; PTR2_2; 1.
 KW Peptide transport; Transport; Transmembrane.
 FT TRANSMEM 91 111 POTENTIAL.
 FT TRANSMEM 116 136 POTENTIAL.
 FT TRANSMEM 154 174 POTENTIAL.
 FT TRANSMEM 200 220 POTENTIAL.
 FT TRANSMEM 228 248 POTENTIAL.
 FT TRANSMEM 351 371 POTENTIAL.
 FT TRANSMEM 387 407 POTENTIAL.
 FT TRANSMEM 431 451 POTENTIAL.
 FT TRANSMEM 472 492 POTENTIAL.
 FT TRANSMEM 511 531 POTENTIAL.
 FT TRANSMEM 556 576 POTENTIAL.
 FT TRANSMEM 585 644 POTENTIAL.
 FT CONFLICT 334 334 R -> ED (IN REF. 2).
 SQ SEQUENCE 585 AA; 64421 MW; C58F8194776E2D97 CRC64;

Query Match 64.4%; Score 38; DB 1; Length 585;
 Best Local Similarity 57.1%; Pred. No. 52;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 WQGYMOV 9
 Db 110 WGRYWTI 116

RESULT 16
 YEJH_ECOLI STANDARD; PRT; 586 AA.
 ID YEJH_ECOLI
 AC P33919; P36926; P36927; P76449;
 DT 01-FEB-1994 (Rel. 28; Created)
 DT 01-NOV-1997 (Rel. 35; Last sequence update)
 DT 01-NOV-1997 (Rel. 35; Last annotation update)
 DE HYPOTHETICAL 66.4 KDA PROTEIN IN RSUA-RPLX INTERGENIC REGION.
 GN YEJH.
 OS Escherichia coli.
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Escherichia.
 OC NCBI_Taxid=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / BHB2600.
 RA Richterich P., Iakey N., Gryan G., Jaehn L., Mintz L., Robison K.,
 RA Church G.M.;
 RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;

RX MEDLINE-97426617; PubMed-9278503;
 RA Blatter F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.,
 RT "The complete genome sequence of *Escherichia coli* K-12.";
 RL Science 277:1453-1474(1997).
 CC -1- SIMILARITY: SOME SIMILARITY TO A PHAGE PROTEIN AND RESTRICTION-
 CC MODIFICATION SYSTEMS.
 CC -1- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS
 CC THAT PRODUCE THREE SEPARATE ORFS.
 CC -----
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 CC -----
 DR EMBL: U00008: AAA16381.1; ALT_FRAME.
 DR EMBL: AE000308: AAC75245.1; -.
 DR EcoGene: EG12045; yehH.
 DR InterPro: IPR001410; -.
 DR InterPro: IPR001650; -.
 DR Pfam: PF00270; DEAD; 1.
 DR Pfam: PF00271; helicase_C; 1.
 DR Hypothetical protein.
 KW Hypothetical protein.
 SQ SEQUENCE 586 AA; 66413 MW; 2D173250F83333DF CRC64;

Query Match 64.4%; Score 38; DB 1; Length 586;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GQYQV 9
 Db 562 GQYQV 567

RESULT 17
 YE68_METYA STANDARD; PRT; 1009 AA.
 AC 058863;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE HYPOTHELICAL PROTEIN MJ1468.
 GN MJ1468.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
 OC Methanococcus.
 ON NCBI_TaxID-2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DSM 2661.
 RX MEDLINE-96337999; PubMed-8688087;
 RA Bolt C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kervelange A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
 RA Uitterlisch T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, *Methanococcus*
 RT *jannaschii*.";
 RL Science 273:1058-1073(1996).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- SIMILARITY: CONTAINS 5 PRD DOMAINS.
 CC -----
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 CC -----
 DR EMBL: U67588: AAB99478.1; -.
 DR TIGR: MJ1468; -.
 DR InterPro: IPR000601; -.
 DR Pfam: PF00801; PKD; 3.
 DR Pfam: PF00801; PKD; 5.
 DR Pfam: PF00801; PKD; 3.
 KW Hypothetical protein; Transmembrane; Repeat.
 FT TRANSMEM 6
 FT TRANSMEM 985 1005
 FT DOMAIN 213 247
 FT DOMAIN 436 503
 FT DOMAIN 724 806
 FT DOMAIN 822 886
 FT DOMAIN 925 962
 FT DOMAIN 293 298
 FT POLY-ASN.
 SQ SEQUENCE 1009 AA; 115119 MW; 13E9B4933EAB7972 CRC64;

Query Match 64.4%; Score 38; DB 1; Length 1009;
 Best Local Similarity 66.7%; Pred. No. 86;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 WGYWQ 8
 Db 322 WGYWQ 327

RESULT 18
 POL_STIVAG STANDARD; PRT; 1046 AA.
 AC P27980;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE POL. POLYPROTEIN (CONTAINS: PROTEASE (RETROPEPSIN) (EC 3.4.23.16);
 DE REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)).
 GN POL.
 OS Simian immunodeficiency virus (AGM3 isolate) (SIY-AGM).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 ON NCBI_TaxID-11730;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-90232731; PubMed-2158689;
 RA Balier M., Garber C., Mueller C., Cichutek K., Kurth R.;
 RT "Complete nucleotide sequence of a simian immunodeficiency virus from
 RT African green monkeys: a novel type of intragroup divergence.";
 RL Virology 176:216-221(1990).
 CC -1- PTM: CLEAVAGE SITES THAT YIELD THE MATURE PROTEINS REMAIN TO BE
 CC DETERMINED.
 CC -1- MISCELLANEOUS: THIS IS AN AFRICAN GREEN MONKEY ISOLATE.
 CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO
 CC KNOWN AS THE RETROPEPSIN FAMILY.
 CC -----
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 CC -----
 DR EMBL: M30931: AAA91914.1; -.
 DR HSSP: P03366; 1HMV.
 DR MEROPS: A02.003; -.
 DR InterPro: IPR000477; -.
 DR InterPro: IPR001037; -.
 DR InterPro: IPR001584; -.
 DR InterPro: IPR001569; -.

DR InterPro: IPR001995; -.
DR InterPro: IPR002156; -.
DR Pfam: PF02022; Integrase_Zn; 1.
DR Pfam: PF00552; Integrase; 1.
DR Pfam: PF00075; rnaaseh; 1.
DR Pfam: PF00665; rve; 1.
DR Pfam: PF00077; rvp; 1.
DR Pfam: PF00078; rvt; 1.
DR PROSITE: PS00141; ASP_PROTEASE; 1.
DR PROSITE: PS00175; ASP_PROT_RETROV; 1.
DR AIDS: Polypotelein; Hydrolase; Aspartyl protease; Endonuclease;
KW Nuclease; Transferase; RNA-directed DNA polymerase.
FT CHAIN 1 195 PROTEASE.
FT ACT_SITE 118 118 BY SIMILARITY.
SQ SEQUENCE 1046 AA; 119328 MW; 9068415C43AD0ACB CRC64;

Query Match 64.4%; Score 38; DB 1; Length 1046;
Best Local Similarity 71.4%; Pred. No. 89;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 WQGYMOV 9
Db 597 WADYMOV 603

RESULT 19
POL_STIVAL STANDARD; PRT; 1047 AA.
ID POL_STIVAL
AC P27973;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE POL. POLYPROTEIN [CONTAINS: PROTEASE (RETROPEPSIN) (EC 3.4.23.16);
DE REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)].
GN POL.
OS Simian immunodeficiency virus (AGM155 isolate) (SIV-AGM).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11727;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90156504; PubMed=2304139;
RA Johnson P.R., Fomsgaard A., Allan J., Gravel M., London W.T.,
RA Olmstead R.A., Hirsch V.M.;
RT "Simian immunodeficiency viruses from African green monkeys display
RT unusual genetic diversity.";
RT J. Virol. 64:1086-1092(1990).
RL J. Virol. 64:1086-1092(1990).
CC -1- PTM: CLEAVAGE SITES THAT YIELD THE MATURE PROTEINS REMAIN TO BE
CC DETERMINED.
CC -1- MISCELLANEOUS: THE 155 ISOLATE IS FROM A MONKEY IMPORTED FROM
CC KENYA.
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO
CC KNOWN AS THE RETROPEPSIN FAMILY.
CC -----
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CC -----
CC EMBL: M29975; AAA91906.1; -.
CC HSSP: P03366; IHMV.
CC MEROPS: A02.003; -.
DR InterPro: IPR000477; -.
DR InterPro: IPR001037; -.
DR InterPro: IPR001584; -.
DR InterPro: IPR001969; -.
DR InterPro: IPR001995; -.
DR InterPro: IPR002156; -.
DR Pfam: PF02022; Integrase_Zn; 1.
DR PROSITE: PS00141; ASP_PROTEASE; 1.
DR PROSITE: PS00175; ASP_PROT_RETROV; 1.

DR Pfam: PF00075; rnaaseh; 1.
DR Pfam: PF00665; rve; 1.
DR Pfam: PF00077; rvp; 1.
DR Pfam: PF00078; rvt; 1.
DR PROSITE: PS00141; ASP_PROTEASE; 1.
DR PROSITE: PS00175; ASP_PROT_RETROV; 1.
DR AIDS: Polypotelein; Hydrolase; Aspartyl protease; Endonuclease;
KW Nuclease; Transferase; RNA-directed DNA polymerase.
FT ACT_SITE 113 113 BY SIMILARITY.
SQ SEQUENCE 1047 AA; 118871 MW; A38DDDA39F268E85 CRC64;

Query Match 64.4%; Score 38; DB 1; Length 1047;
Best Local Similarity 71.4%; Pred. No. 89;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 WQGYMOV 9
Db 592 WADYMOV 598

RESULT 20
POL_STIVAL STANDARD; PRT; 1057 AA.
ID POL_STIVAL
AC Q02836;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE POL. POLYPROTEIN [CONTAINS: PROTEASE (RETROPEPSIN) (EC 3.4.23.16);
DE REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)].
GN POL.
OS Simian immunodeficiency virus (isolate AGM / clone GRI-1) (SIV-AGM).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=31684;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91220680; PubMed=2024476;
RA Fomsgaard A., Hirsch V.M., Allan J.S., Johnson P.R.;
RA "A highly divergent proviral DNA clone of SIV from a distinct species
RT of African green monkey.";
RT Virology 182:397-402(1991).
RL Virology 182:397-402(1991).
CC -1- PTM: CLEAVAGE SITES THAT YIELD THE MATURE PROTEINS REMAIN TO BE
CC DETERMINED.
CC -1- MISCELLANEOUS: THIS IS AN AFRICAN GREEN MONKEY ISOLATE.
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO
CC KNOWN AS THE RETROPEPSIN FAMILY.
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CC -----
CC EMBL: M66437; AAA91923.2; -.
CC EMBL: M58410; CAB26041.1; -.
CC HSSP: P03366; IHMV.
CC MEROPS: A02.003; -.
DR InterPro: IPR000477; -.
DR InterPro: IPR001037; -.
DR InterPro: IPR001584; -.
DR InterPro: IPR001969; -.
DR InterPro: IPR001995; -.
DR InterPro: IPR002156; -.
DR Pfam: PF02022; Integrase_Zn; 1.
DR Pfam: PF00552; Integrase; 1.
DR Pfam: PF00075; rnaaseh; 1.
DR Pfam: PF00665; rve; 1.
DR Pfam: PF00077; rvp; 1.
DR Pfam: PF00078; rvt; 1.
DR PROSITE: PS00141; ASP_PROTEASE; 1.
DR PROSITE: PS00175; ASP_PROT_RETROV; 1.

KW AIDS: Polyprotein; Hydrolase; Aspartyl protease; Endonuclease;
 KW Nuclease; Transferase; RNA-directed DNA polymerase.
 FT ACT_SITE 114 114 BY SIMILARITY.
 SQ SEQUENCE 1057 AA; 120566 MW; 0550E954011FAA2C CRC64;

Query Match 64.4%; Score 38; DB 1; Length 1057;
 Best Local Similarity 62.5%; Pred. NO. 89;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTWGQYWG 8
 ||| :||
 Db 590 KTWDMWVQ 597

RESULT 21
 ID POL_SIVAT STANDARD; PRT; 1061 AA.
 AC P05895;
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DE 30-MAY-2000 (Rel. 39, Last annotation update)
 DE POLYPROTEIN [CONTAINS: PROTEASE (RETROPEPSIN) (EC 3.4.23.16);
 DE REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)]
 GN POL.
 OS Simian immunodeficiency virus (TWO-1 isolate) (STV-AGM).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11731;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88232906; PubMed=3374586;
 RA Fukasawa M., Mura T., Hasegawa A., Morikawa S., Tsujimoto H.,
 RA Miki K., Kitamura T., Hayami M.;
 RT "Sequence of simian immunodeficiency virus from African green monkey,
 RT a new member of the HIV/SIV group."
 RL Nature 333:457-461(1988).
 CC -1 PTM: CLEAVAGE SITES THAT YIELD THE MATURE PROTEINS REMAIN TO BE
 CC DETERMINED.
 CC -1 MISCELLANEOUS: THIS IS AN AFRICAN GREEN MONKEY ISOLATE.
 CC -1 SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO
 CC KNOWN AS THE RETROPEPSIN FAMILY.
 CC -----
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 CC -----
 CC EMBL: X07805; CAA30658.1; ALT_SEQ.
 DR PIR: B30045; GNLAG4.
 DR HSSP: P03366; IMHV.
 DR HIV: X07805; POLSAGMTY.
 DR MEROPS: A02.003; -;
 DR InterPro: IPR000477; -;
 DR InterPro: IPR001037; -;
 DR InterPro: IPR001584; -;
 DR InterPro: IPR001969; -;
 DR InterPro: IPR002156; -;
 DR Pfam: PF02022; Integrase_Zn; 1.
 DR Pfam: PF00552; Integrase_Zn; 1.
 DR Pfam: PF00075; rnaaseH; 1.
 DR Pfam: PF00665; rve; 1.
 DR Pfam: PF00077; rvp; 1.
 DR Pfam: PF00078; rvt; 1.
 DR PROSITE: PS00141; ASP_PROTEASE; 1.
 DR PROSITE: PS50175; ASP_PROT_RETROV; 1.
 KW AIDS: Polyprotein; Hydrolase; Aspartyl protease; Endonuclease;
 KW Nuclease; Transferase; RNA-directed DNA polymerase.
 FT CHAIN 1 210
 FT ACT_SITE 134 134 BY SIMILARITY.

SO SEQUENCE 1061 AA; 120612 MW; 13DDDA104CB432A4 CRC64;

Query Match 64.4%; Score 38; DB 1; Length 1061;
 Best Local Similarity 71.4%; Pred. NO. 90;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 WQYQVQV 9
 |||||
 Db 613 WADYQVQV 619

RESULT 22
 ID UBIA_ECOLI STANDARD; PRT; 290 AA.
 AC P26601;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE 4-HYDROXYBENZONATE OCTAPRENYLTRANSFERASE (EC 2.5.1.-) (4-HB
 DE POLYPRENYLTRANSFERASE).
 GN UBIA OR CYR.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92355505; PubMed=1644758;
 RA Nichols B.P., Green J.M.;
 RT "Cloning and sequencing of Escherichia coli ublc and purification of
 RT chorismate lyase."
 RL J. Bacteriol. 174:5309-5316(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=K12 / MC4100;
 RX MEDLINE=92354744; PubMed=1644192;
 RA Siebert M., Bechtold A., Meizer M., May U., Berger U., Schroeder G.,
 RA Schroeder J., Severin K., Heide U.;
 RT "Ubiquinone biosynthesis. Cloning of the genes coding for chorismate
 RT pyruvate-lyase and 4-hydroxybenzoate octaprenyl transferase from
 RT Escherichia coli."
 RL FEBS Lett. 307:347-350(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN=K12 / W3110;
 RX MEDLINE=92380960; PubMed=1512213;
 RA Nishimura K., Nakahigashi K., Inokuchi H.;
 RT "Location of the ubia gene on the physical map of Escherichia coli."
 RL J. Bacteriol. 174:5762-5762(1992).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX STRAIN=K12;
 RA Wolter F.P.;
 RL Submitted (NOV-1992) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX STRAIN=K12 / MG1655;
 RX MEDLINE=94089392; PubMed=8265357;
 RA Blatner F.R., Burland V.D., Plunkett G. III, Sofia H.J.,
 RA Daniels D.L.;
 RT "Analysis of the Escherichia coli genome. IV. DNA sequence of the
 RT region from 89.2 to 92.8 minutes."
 RL Nucleic Acids Res. 21:5408-5417(1993).
 RN [6]
 RP SEQUENCE OF 1-80 FROM N.A.
 RX STRAIN=K12;
 RX MEDLINE=94014977; PubMed=8409922;
 RX Wu G., Williams H.D., Gibson F., Poole R.K.;
 RT "Mutants of Escherichia coli affected in respiration: the cloning and
 RT nucleotide sequence of ubia, encoding the membrane-bound p-
 RT hydroxybenzoate:octaprenyltransferase.";

RL J. Gen. Microbiol. 139:1795-1805(1993).
 RN (17)
 RP CHARACTERIZATION.
 RX MEDLINE=94207029; PubMed=8155731;
 RA Melzer M., Heide L.;
 RT "Characterization of polyphosphatase: 4-hydroxybenzoate
 RT polyphosphatase from *Escherichia coli*.";
 RL Polchim. Biophys. Acta 1212:93-107(1994).
 RN (8)
 RP CHARACTERIZATION.
 RX MEDLINE=95072311; PubMed=765507;
 RA Suzuki K., Ueda M., Yuasa M., Nakagawa T., Kawamukai M., Matsuda H.;
 RT "Evidence that *Escherichia coli* ubia product is a functional homolog
 RT of yeast COQ2, and the regulation of ubia gene expression.";
 RL Biosci. Biotechnol. Biochem. 58:1814-1819(1994).
 CC -1- FUNCTION: SYNTHESIS OF 3-OCTAPRENYL-4-HYDROXYBENZOATE.
 CC -1- CATALYTIC ACTIVITY: 4-HYDROXYBENZOATE + FARNESYLFARNESYLGERANIOL
 CC -3-OCTAPRENYL-4-HYDROXYBENZOATE.
 CC -1- COFACTOR: REQUIRES MAGNESIUM.
 CC -1- PATHWAY: SECOND STEP IN UBIQUINONE BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
 CC -1- SIMILARITY: BELONGS TO THE UBIA PRENYLTRANSFERASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; M93136; AAA24712.1; -
 DR EMBL; M93413; AAA24717.1; -
 DR EMBL; X66619; CAA47182.1; -
 DR EMBL; X57434; CAA40682.1; -
 DR EMBL; X69522; CAA49270.1; -
 DR EMBL; U00006; AAC43134.1; -
 DR EMBL; AE000477; AAC77010.1; -
 DR EMBL; M96268; AAA17028.1; -
 DR EMBL; X63407; CAA45003.1; -
 DR PIR; B42956; B42956.
 DR PIR; S24361; S24361.
 DR PIR; S25661; S25661.
 DR PIR; S31432; S31432.
 DR PIR; JC2316; JC2316.
 DR Ecogene; EG11370; ubia.
 DR InterPro; IPR000537; -
 DR Pfam; PF01040; Ubia; 1.
 DR PROSITE; PS00943; Ubia; 1.
 KW Ubiquinone biosynthesis; Transferase; Transmembrane; Inner membrane;
 KW Magnesium.
 FT TRANSMEM 23 43 POTENTIAL.
 FT TRANSMEM 46 66 POTENTIAL.
 FT TRANSMEM 100 120 POTENTIAL.
 FT TRANSMEM 141 161 POTENTIAL.
 FT TRANSMEM 163 183 POTENTIAL.
 FT TRANSMEM 213 233 POTENTIAL.
 FT TRANSMEM 234 254 POTENTIAL.
 FT TRANSMEM 268 288 POTENTIAL.
 SQ SEQUENCE 290 AA; 32511 MW; F10PEDID7A30E115 CRC64;

Query Match 62.7%; Score 37; DB 1; Length 290;
 Best Local Similarity 57.1%; Pred. No. 39;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 WGYWCV 9
 DB 237 WGYWCV 243

RESULT 23
 SLEB_BACSU

ID SLEB_BACSU STANDARD; PRT; 305 AA.
 AC P50739;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE SPORE-CORTEX-LYTIC ENZYME PRECURSOR.
 GN SLEB.
 OS *Bacillus subtilis*.
 OC Bacteria; Firmicutes; *Bacillus*/Clostridium group;
 OC *Bacillus*/Staphylococcus group; *Bacillus*.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=96427343; PubMed=8830707;
 RA Moriyma R., Hattori A., Miyata S., Kudoh S., Makino S.;
 RT "A gene (sleb) encoding a spore cortex-lytic enzyme from *Bacillus*
 RT subtilis and response of the enzyme to L-alanine-mediated
 RT germination";
 RL J. Bacteriol. 178:6059-6063(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168 / MARBURG;
 RX MEDLINE=96349105; PubMed=8760912;
 RA Sorokin A.V., Azevedo V., Zumbstein E., Galleron N., Ehrlich S.D.,
 RA Serror P.;
 RT "Sequence analysis of the *Bacillus subtilis* chromosome region between
 RT the *serA* and *kdg* loci cloned in a yeast artificial chromosome";
 RL Microbiology 142:2005-2016(1996).
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 CC -----
 DR EMBL; D79978; BAA11473.1; -
 DR EMBL; L47648; AAC83957.1; -
 DR EMBL; Z99115; CAB14209.1; -
 DR EMBL; Z99116; CAB14225.1; -
 DR Subtilist; BG11439; sleb.
 DR InterPro; IPR002477; -
 DR Pfam; PF01471; PG_binding_1; 1.
 KW Signal.
 FT SIGNAL 1 29 POTENTIAL.
 FT CHAIN 30 305 SPORE-CORTEX-LYTIC ENZYME.
 SQ SEQUENCE 305 AA; 34001 MW; 9DF1305975F5BE16 CRC64;

Query Match 62.7%; Score 37; DB 1; Length 305;
 Best Local Similarity 71.4%; Pred. No. 41;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 WGYWCV 9
 DB 67 WGYWCV 73

RESULT 24
 LIP3_DROME
 LIP3_DROME STANDARD; PRT; 394 AA.
 AC O46108;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE LIPASE 3 PRECURSOR (EC 3.1.1.-).
 GN LIP3 OR CG8823.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydriidae; *Drosophillidae*; *Drosophila*.

OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CANTON-S;
 RX MEDLINE=98227313; PubMed=9566193;
 RA Pistillo D., Manzi A., Tino A., Pilo Boyl P., Graziani F., Malva C.;
 RT "The *Drosophila melanogaster* lipase homologs: a gene family with
 tissue and developmental specific expression.";
 RL J. Mol. Biol. 276:877-885(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanalides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brannon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Berns P.V., Bernier B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,
 RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Hock J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kenton J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lal Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mekulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svrstka R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 CC -1- TISSUE SPECIFICITY: FMT BODY.
 CC -1- DEVELOPMENTAL STAGE: ONLY AT CANAL STAGES.
 CC -1- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
 CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.). ALSO SIMILAR TO
 CC LIPIDOPROTEIN EGG-SPECIFIC AND YOLK PROTEINS.
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 CC
 CC EMBL: Y14367; CAAT74737.1;
 CC EMBL: AE003699; AAF54935.1;
 CC FLYBASE: FBgn0023495; Lip3.
 CC InterPro: IPR000073;
 CC InterPro: IPR000379;
 CC InterPro: IPR000734;
 CC Pfam: PF00561; abhydrolase_1.
 CC PROSITE: PS00120; LIPASE_SER; 1.

KW Hydrolase; Lipid degradation; Signal; Glycoprotein.
 FT SIGNAL 1 20
 FT CHAIN 21 394
 FT ACT_SITE 164 164
 FT ACT_SITE 369 369
 FT CARBOHYD 131 131
 FT SEQUENCE 394 AA; 44901 MW; A718D1D743673802 CRC64;
 Query Match 62.7%; Score 37; DB 1; Length 394;
 Best Local Similarity 55.6%; Pred. No. 52;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 OY 1 KTWGQYMW 9
 DB 120 KTWGQYMW 128
 RESULT 25
 YFE9_YEAST STANDARD; PRT; 623 AA.
 AC P43534;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE HYPOTHETICAL 70.3 KDA PROTEIN IN ALR2-EMP47 INTERGENIC REGION.
 GN YFL049W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RX MEDLINE=95400292; PubMed=7670463;
 RA Murakami Y., Natou M., Hagiwara H., Shibata T., Ozawa M.,
 RA Sasakura S.-I., Sasakura M., Tsuchiya Y., Soeda E., Yokoyama K.,
 RA Yamazaki M., Tashiro H., Eki T.;
 RT "Analysis of the nucleotide sequence of chromosome VI from
 RT Saccharomyces cerevisiae.";
 RL Nat. Genet. 10:261-268(1995).
 CC -1- SIMILARITY: TO YEAST NPL6.
 CC
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 CC
 CC EMBL: D50617; BAA09192.1;
 CC SGD: S0001845; YFL049W.
 CC KW Hypothetical protein.
 CC SEQUENCE 623 AA; 70275 MW; ABAAC00CAC8F0ED0E CRC64;
 Query Match 62.7%; Score 37; DB 1; Length 623;
 Best Local Similarity 62.5%; Pred. No. 78;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 OY 1 KTWGQYMW 8
 DB 491 KTWGQYMW 498
 RESULT 26
 YD64_MYCPN STANDARD; PRT; 677 AA.
 AC P75417;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE HYPOTHETICAL PROTEIN MPN364 (H91_ORF677).
GN MPN364 OR MP472.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelfreih R., Hilbert H., Plagens H., Pirk E., Li B.-C.,
Herrmann R.,
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
pneumoniae.";
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -1- SIMILARITY: BELONGS TO THE MG185 / MG260 FAMILY.
CC -----
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CC -----
DR EMBL: AE000047; AAB96120.1; -.
KW Hypothetical protein.
SQ SEQUENCE 677 AA; 75591 MW; E785B68BD679F04D CRC64;

Query Match 62.7%; Score 37; DB 1; Length 677;
Best Local Similarity 66.7%; Pred. No. 85;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTWGQYMOV 9
GN 153 KTWGQYMOV 161
DB 153 KTWGQYMOV 161

RESULT 27
POL_HV2CA STANDARD; PRT; 1034 AA.
ID POL_HV2CA
AC P24107;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE POL. POLYPROTEIN (CONTAINS: PROTEASE (RETROPEPSIN) (EC 3.4.23.16);
DE REVERSE TRANSCRIPTION (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)).
GN POL.
OS Human immunodeficiency virus type 2 (isolate CAM2) (HIV-2).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11715;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91170959; PubMed=2005437;
RA Tristem M., Hill F., Karpas A.,
RT "Nucleotide sequence of a guinea-Bissau-derived human
RT immunodeficiency virus type 2 proviral clone (HIV-2CAM2).";
RL J. Gen. Virol. 72:721-724(1991).
CC -1- PTM: CLEAVAGE SITES THAT YIELD THE MATURE PROTEINS REMAIN TO BE
CC DETERMINED.
CC -----
CC -1- MISCELLANEOUS: READTHROUGH OF THE TERMINATOR TGA MAY OCCUR BETWEEN
CC 564-TLE AND 565-GLY.
CC -----
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO
CC KNOWN AS THE RETROPEPSIN FAMILY.
CC -----
DR PIR: B38475; GNLJCA.
DR HSSP: P04584; LJIJD.
DR MEROPS: A02.002;
DR InterPro: IPR000477; -.
DR InterPro: IPR001037; -.
DR InterPro: IPR001584; -.
DR InterPro: IPR001699; -.
DR InterPro: IPR001955; -.

DR InterPro: IPR002156; -.
DR Pfam: PF02022; Integrase; Zn. 1.
DR Pfam: PF00552; Integrase; 1.
DR Pfam: PF00075; rnses; 1.
DR Pfam: PF00665; rve; 1.
DR Pfam: PF00077; rvp; 1.
DR Pfam: PF00078; rvc; 1.
DR PROSITE: PS00141; ASP_PROTEASE; 1.
DR PROSITE: PS00175; ASP_PROT_RETROV; 1.
KW AIDS; Polypeptide; Hydrolase; Aspartyl protease; Endonuclease;
KW Nuclease; Transferase; RNA-directed DNA polymerase.
FT CHAIN 85
FT ACT_SITE 109
SQ SEQUENCE 1034 AA; 117195 MW; 3514E566AA6D7C86 CRC64;

Query Match 62.7%; Score 37; DB 1; Length 1034;
Best Local Similarity 71.4%; Pred. No. 1,2e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 MGQYMOV 9
GN 583 MGQYMOV 589
DB 583 MGQYMOV 589

RESULT 28
POL_HV2KR STANDARD; PRT; 1035 AA.
ID POL_HV2KR
AC Q74120;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE POL. POLYPROTEIN (CONTAINS: PROTEASE (RETROPEPSIN) (EC 3.4.23.16);
DE REVERSE TRANSCRIPTION (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)).
GN POL.
OS Human immunodeficiency virus type 2 (isolate KR) (HIV-2).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=73484;
RN [1]
RP SEQUENCE FROM N.A.
RA Kraus G.K., Talbot R., Leavitt M., Luzznick L., Schmidt A.,
RA Badel P., Bartz C., Morton W., Wong-Staal F., Looney D.J.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBD databases.
CC -1- PTM: CLEAVAGE SITES THAT YIELD THE MATURE PROTEINS REMAIN TO BE
CC DETERMINED.
CC -----
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO
CC KNOWN AS THE RETROPEPSIN FAMILY.
CC -----
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CC -----
DR EMBL: U22047; AAA64576.1; -.
DR HSSP: P04584; LJIJD.
DR InterPro: IPR000477; -.
DR InterPro: IPR001037; -.
DR InterPro: IPR001584; -.
DR InterPro: IPR001969; -.
DR InterPro: IPR001995; -.
DR InterPro: IPR002156; -.
DR Pfam: PF02022; Integrase; Zn. 1.
DR Pfam: PF00552; Integrase; 1.
DR Pfam: PF00075; rnses; 1.
DR Pfam: PF00665; rve; 1.
DR Pfam: PF00077; rvp; 1.
DR Pfam: PF00078; rvc; 1.
DR PROSITE: PS00141; ASP_PROTEASE; 1.
DR PROSITE: PS00175; ASP_PROT_RETROV; 1.
KW AIDS; Polypeptide; Hydrolase; Aspartyl protease; Endonuclease;
KW AIDS; Polypeptide; Hydrolase; Aspartyl protease; Endonuclease;

KW Nuclease; Transferase; RNA-directed DNA polymerase.
 FT CHAIN 85 183 PROTEASE.
 FT ACT SITE 109 109 BY SIMILARITY
 SQ SEQUENCE 1035 AA; 117632 MW; 696E6DC6CAFB06CF CRC64;

Query Match 62.7%; Score 37; DB 1; Length 1035;
 Best Local Similarity 71.4%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 WGOYMOV 9
 Db 584 WDNWMOV 590

RESULT 29
 ID POL_HV2NZ STANDARD; PRT; 1035 AA.
 AC P05962; Q85571;
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE POL POLYPROTEIN [CONTAINS: PROTEASE (RETROPEPSIN) (EC 3.4.23.16);
 DE REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)]
 GN POL.
 OS Human immunodeficiency virus type 2 (isolate NIH-2) (HIV-2).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11719;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88320359; PubMed=1261862;
 RA Zagury J.F., Franchini G., Reitz M.S. Jr., Collalti E., Starchich B.R.,
 RA Hall L., Fargnoli K., Jagodzinski L.L., Guo H.-G., Laure F.,
 RA Ayra S.K., Josephs S.F., Zagury D., Wong-Staal F., Gallo R.C.;
 RT "Genetic variability between isolates of human immunodeficiency virus
 (HIV) type 2 is comparable to the variability among HIV type 1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:5941-5945(1988).
 CC -1- PWM: CLEAVAGE SITES THAT YIELD THE MATURE PROTEINS REMAIN TO BE
 CC DETERMINED.
 CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO
 CC KNOWN AS THE RETROPEPSIN FAMILY.
 CC -----
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 CC -----
 DR EMBL: J03654; AAB00755.1; ALT_INT.
 DR HSSP: P04584; 1JLD.
 DR HIV: J03654; POLS2NINZ.
 DR MEROPS: A02.002; -
 DR InterPro: IPR000477; -
 DR InterPro: IPR001037; -
 DR InterPro: IPR001584; -
 DR InterPro: IPR001969; -
 DR InterPro: IPR001995; -
 DR InterPro: IPR002156; -
 DR Pfam: PF02022; Integrase_2n; 1.
 DR Pfam: PF00052; Integrase; 1.
 DR Pfam: PF00075; rnaaseh; 1.
 DR Pfam: PF00655; rve; 1.
 DR Pfam: PF00077; rvp; 1.
 DR Pfam: PF00078; rvt; 1.
 DR PROSITE: PS00141; ASP_PROTASE; FALSE_NEG.
 DR PROSITE: PS00175; ASP_PROT_RETROV; 1.
 KW AIDS: Polypeptide; Hydrolase; Aspartyl protease; Endonuclease;
 KW Nuclease; Transferase; RNA-directed DNA polymerase.
 FT CHAIN 85 183 PROTEASE.
 FT ACT_SITE 109 109 BY SIMILARITY.
 SQ SEQUENCE 1035 AA; 117323 MW; E3DC4E2DF457F6BA CRC64;

Query Match 62.7%; Score 37; DB 1; Length 1035;
 Best Local Similarity 71.4%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 WGOYMOV 9
 Db 584 WDNWMOV 590

RESULT 30
 ID POL_HV2SB STANDARD; PRT; 1035 AA.
 AC P12451; Q85570;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE POL POLYPROTEIN [CONTAINS: PROTEASE (RETROPEPSIN) (EC 3.4.23.16);
 DE REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)]
 GN POL.
 OS Human immunodeficiency virus type 2 (isolate SBLISY) (HIV-2).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11718;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89184641; PubMed=2648404;
 RA Franchini G., Fargnoli K.A., Giombini F., Jagodzinski L., de Rossi A.,
 RA Bosch M., Biberfeld G., Fenyo A.M., Albert J., Gallo R.C.,
 RA Wong-Staal F.;
 RT "Molecular and biological characterization of a replication competent
 RT human immunodeficiency type 2 (HIV-2) proviral clone.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:2433-2437(1989).
 CC -1- PWM: CLEAVAGE SITES THAT YIELD THE MATURE PROTEINS REMAIN TO BE
 CC DETERMINED.
 CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO
 CC KNOWN AS THE RETROPEPSIN FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: J04498; AAB00746.1; ALT_INT.
 DR HSSP: P04584; 1JLD.
 DR HIV: J04498; POLS2ISY.
 DR MEROPS: A02.002; -
 DR InterPro: IPR000477; -
 DR InterPro: IPR001037; -
 DR InterPro: IPR001584; -
 DR InterPro: IPR001969; -
 DR InterPro: IPR001995; -
 DR InterPro: IPR002156; -
 DR Pfam: PF02022; Integrase_2n; 1.
 DR Pfam: PF00052; Integrase; 1.
 DR Pfam: PF00075; rnaaseh; 1.
 DR Pfam: PF00655; rve; 1.
 DR Pfam: PF00077; rvp; 1.
 DR Pfam: PF00078; rvt; 1.
 DR PROSITE: PS00141; ASP_PROTASE; 1.
 DR PROSITE: PS00175; ASP_PROT_RETROV; 1.
 KW AIDS: Polypeptide; Hydrolase; Aspartyl protease; Endonuclease;
 KW Nuclease; Transferase; RNA-directed DNA polymerase.
 FT CHAIN 85 183 PROTEASE.
 FT ACT_SITE 109 109 BY SIMILARITY.
 SQ SEQUENCE 1035 AA; 117552 MW; 9DA9BD9DBE4393 CRC64;

Query Match 62.7%; Score 37; DB 1; Length 1035;
 Best Local Similarity 71.4%; Pred. No. 1.2e+02;

Matches	5;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
QY	3	WGOYWOY	9						
Db	584	WDNYWOY	590						

Search completed: July 3, 2001, 10:28:38
Job time: 323 sec

7

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2001, 10:23:58 ; Search time 33.34 Seconds
(without alignments)
16.365 Million cell updates/sec

Title: US-09-214-836-9

Sequence: 1 KTWGQYQGV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq_0601:*

- 1: /SIDSR/gcgdata/geneseq/geneseq/AA1980.DAT:*
- 2: /SIDSR/gcgdata/geneseq/geneseq/AA1981.DAT:*
- 3: /SIDSR/gcgdata/geneseq/geneseq/AA1982.DAT:*
- 4: /SIDSR/gcgdata/geneseq/geneseq/AA1983.DAT:*
- 5: /SIDSR/gcgdata/geneseq/geneseq/AA1984.DAT:*
- 6: /SIDSR/gcgdata/geneseq/geneseq/AA1985.DAT:*
- 7: /SIDSR/gcgdata/geneseq/geneseq/AA1986.DAT:*
- 8: /SIDSR/gcgdata/geneseq/geneseq/AA1987.DAT:*
- 9: /SIDSR/gcgdata/geneseq/geneseq/AA1988.DAT:*
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- 11: /SIDSR/gcgdata/geneseq/geneseq/AA1990.DAT:*
- 12: /SIDSR/gcgdata/geneseq/geneseq/AA1991.DAT:*
- 13: /SIDSR/gcgdata/geneseq/geneseq/AA1992.DAT:*
- 14: /SIDSR/gcgdata/geneseq/geneseq/AA1993.DAT:*
- 15: /SIDSR/gcgdata/geneseq/geneseq/AA1994.DAT:*
- 16: /SIDSR/gcgdata/geneseq/geneseq/AA1995.DAT:*
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- 18: /SIDSR/gcgdata/geneseq/geneseq/AA1997.DAT:*
- 19: /SIDSR/gcgdata/geneseq/geneseq/AA1998.DAT:*
- 20: /SIDSR/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 21: /SIDSR/gcgdata/geneseq/geneseq/AA2000.DAT:*
- 22: /SIDSR/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	9	16	AA78644
2	59	100.0	9	19	AAW77119
3	59	100.0	9	19	AAW7850
4	59	100.0	9	19	AAW70010
5	59	100.0	9	19	AAW54598
6	59	100.0	9	19	AAW5770
7	59	100.0	9	20	AAV49663
8	59	100.0	9	20	AAV53524
9	59	100.0	9	20	AAV47616
10	59	100.0	9	20	AAV33172
11	59	100.0	9	20	AAV40211

12	59	100.0	9	20	AAV26867	Melanoma-derived 1
13	59	100.0	9	20	AAV01753	Exemplary antigen
14	59	100.0	9	20	AAV00715	Tumour antigen bco
15	59	100.0	9	20	AAV10449	HLA Class I motif
16	59	100.0	9	21	AAV33662	MHC class I associ
17	59	100.0	9	21	AAV33679	Cytotoxic T lympho
18	59	100.0	9	21	AAV08694	Antigenic peptide
19	59	100.0	9	21	AAV71520	Human gp100 Pmel1
20	59	100.0	9	21	AAV02622	Tumour associated
21	59	100.0	9	21	AAV90803	Human leukocyte an
22	59	100.0	9	21	AAV92299	gp100-Pmel17 anti
23	59	100.0	9	21	AAV84296	Tumour associated
24	59	100.0	9	21	AAV82979	gp100(Pmel117) tum
25	59	100.0	9	21	AAV56641	gp100-Pmel117 gen
26	59	100.0	9	22	AAV31354	Exemplary antigen
27	59	100.0	10	16	AAV8643	Immunogenic peptid
28	59	100.0	10	16	AAV84209	gp100 melanoma ant
29	59	100.0	11	16	AAV8642	Immunogenic peptid
30	59	100.0	30	22	AAV61647	gp100 peptide #1.
31	59	100.0	661	16	AAV84855	MART-1 melanoma an
32	59	100.0	661	16	AAV8646	Melanoma associate
33	59	100.0	661	20	AAV31977	Human melanoma ant
34	59	100.0	662	20	AAV42627	Human melanoma ant
35	59	100.0	668	18	AAV38164	Pmel17 encoded by
36	55	93.2	9	19	AAV42542	Gp 100 epitope (re
37	55	93.2	625	20	AAV31978	Mouse melanoma ant
38	55	93.2	661	16	AAV84854	MART-1 melanoma an
39	54	91.5	8	16	AAV8641	Immunogenic peptid
40	54	91.5	9	16	AAV8645	Immunogenic peptid
41	54	91.5	9	16	AAV84804	Modified MART-1 me
42	54	91.5	9	16	AAV84805	Modified MART-1 me
43	54	91.5	9	16	AAV84806	Modified MART-1 me
44	54	91.5	9	16	AAV84807	Modified MART-1 me
45	54	91.5	9	16	AAV84808	Modified MART-1 me

ALIGNMENTS

RESULT 1	
AAV8644	AAV8644 standard; Protein; 9 AA.
XX	
AC	AAV8644;
XX	
DT	22-JAN-1996 (first entry)
XX	
DE	Immunogenic peptide of melanoma associated antigen gp100.
KW	Melanoma: antigen; vaccine; immunogen; primer; probe; detection;
KW	identification; tumour; gp100.
XX	
OS	Homo sapiens.
XX	
PN	EP68350-A1.
XX	
XX	23-AUG-1995.
PD	
XX	
PF	14-FEB-1995; 95EP-0200348.
XX	
XX	21-DEC-1994; 94EP-0203709.
PR	16-FEB-1994; 94EP-0200337.
PA	
XX	(ALKU) AKZO NOBEL NV.
PI	Adema GJ, Fligdor CG;
XX	
DR	WPI: 1995-284790/38.
XX	N-PSDB: AAQ96055.
XX	
PT	Melanoma associated antigen gp100 - used in vaccines and for the
PF	detection of tumours
XX	

PS Claim 5; Page 31; 40pp; English.

XX Immunogenic peptides derived from the melanoma associated antigen
CC (See AAR78639-45) may be used in the production of vaccines.
CC Nucleotide sequences encoding the immunogenic peptides may be used
CC as primers and probes in the detection of melanoma cells. Tumour
CC infiltrating lymphocytes capable of binding to the melanoma
CC associated antigen can be cultured ex vivo and returned to melanoma
CC particles, and when radiolabelled, they may be used to identify
CC tumour deposits.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 59; DB 16; Length 9;

Best Local Similarity 100.0%; Pred. No. 3.4e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KTWGOTMOV 9
| | | | |
DB 1 ktwgqywyv 9

RESULT 2

AAW77119
ID AAW77119 standard; peptide; 9 AA.

XX AAW77119;

DT 16-NOV-1998 (first entry)

DE gp100/Pmel17 synthetic peptide epitope 1.

XX Tyrosinase; tyrosinase cytotoxic lymphocyte response;

KW cytotoxic T lymphocyte; cysteine-depleted; melanoma.

XX Synthetic.

PN WO9833810-A2.

PD 06-AUG-1998.

PF 29-JAN-1998; 98WO-US01592.

PR 30-JAN-1997; 97US-0037781.

PA (UYVI-) UNIV VIRGINIA PATENT FOUND.

PI Engelhard VH, Hunt DF, Kittlesen D, Slingluff CL;

DR WPI; 1998-437388/37.

XX Disease specific immunogen - comprises disease specific cytotoxic T
PT lymphocyte epitope used to elicit melanoma specific CTL response

XX Disclosure; Page 27; 93pp; English.

XX The peptide epitope AAW77119-W77138 were created for human
CC tumour-specific cytotoxic T lymphocyte response. These peptides are
CC cysteine- depleted mutants of a native disease-specific CTL epitope. The
CC response than the native epitope. The epitopes can be used in a
CC disease-specific immunogen to protect a mammal against disease in
CC particular melanomas. The peptides may also be used to screen a sample
CC for the presence of an antigen with the same epitope, or with a different
CC cross-reactive epitope.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 59; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KTWGOTMOV 9
| | | | |
DB 1 ktwgqywyv 9

RESULT 3

AAW78850
ID AAW78850 standard; peptide; 9 AA.

XX AAW78850;

DT 17-NOV-1998 (first entry)

DE PMEL 17 (gp100) protein fragment 154-162.

XX Microparticle; delivery; polymeric matrix; autoantigen; tumour antigen;
KW class II associated peptide; pathogen; gene therapy; genetic disease;
KW infection; downregulation; immune response.

XX Homo sapiens.

OS Synthetic.

PN WO9831398-A1.

PD 23-JUL-1998.

PF 22-JAN-1998; 98WO-US01499.

PR 06-JAN-1998; 98US-0003253.

PR 22-JAN-1997; 97US-0787547.

PA (PANG-) PANGAEA PHARM INC.

PI Curley JM, Hedley ML, Langer RS, Lunsford LB;

DR WPI; 1998-427556/36.

XX New preparations of microparticles - comprising a synthetic polymer
PT matrix and nucleic acid comprising an expression vector for use in
PT gene therapy
XX
PS Disclosure; Page 10; 101pp; English.

XX A microparticle preparation (MP) has been developed, consisting of
CC microparticles having a diameter of less than 100 mu m. The MP
CC comprises: (a) a polymeric matrix (PM) consisting of one or more
CC synthetic polymers having a solubility in water of less than 1 mg/L; and
CC (b) an expression vector selected from RNA molecules (at least 50% of
CC which are closed circles) or circular plasmid DNA (at least 50% of which
CC are supercoiled). Also described is a MP of at most 20 microns in
CC diameter, comprising: (a) a PM; and (b) a NM comprising an expression
CC control sequence operatively linked to a coding sequence, where the
CC coding sequence encodes an expression product selected from: (1) a
CC polypeptide at least 7 amino acids in length, having a sequence identical
CC to the sequence of: (i) a fragment of a naturally-occurring mammalian
CC protein; or (ii) a fragment of a naturally-occurring protein from an
CC infectious agent which infects a mammal; (2) a peptide having a length
CC and sequence which permits it to bind to an MHC class I or II molecule;
CC and (3) the polypeptide or the peptide linked to a trafficking sequence.
CC AAW69763 to AAW69765, and AAW78793 to AAW78897 are peptide fragments for
CC use in the present invention. The MPs are highly effective vehicles for
CC the delivery of polynucleotides into phagocytic cells. They can be used
CC for gene therapy, e.g. for treating genetic diseases, infections or
CC tumours or for downregulating an immune response.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 59; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTWGQYMOV 9
 |||||
 Db 1 ktwgqyqv 9

RESULT 4

AAW70010
 ID AAW70010 standard; peptide; 9 AA.

AC AAW70010;

DT 22-OCT-1998 (first entry)

DE Melanoma-associated antigen gp100 derived HLA-A2.1 binding peptide 1.

XX Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW human leukocyte antigen; HLA; tumour associated antigen; cancer;
 KW antigen presenting cell; APC; immunogenic peptide; immune disorder;
 KW viral infection; AIDS; hepatitis; bacterial infection; malaria;
 KW fungal infection; tuberculosis; melanoma; gp100.

OS Synthetic.
 OS Homo sapiens.

PN W09833888-A1.

PD 06-AUG-1998.

PF 30-JAN-1998; 98WO-D501959.

PR 31-JAN-1997; 97US-0036696.

PA (EPIM-) EPIMMUNE INC.

PI Celis E, Sette A, Sidney J, Southwood S, Tsai V;

DR WPI; 1998-437445/37.

PT Production of antigen-specific cytotoxic T cells - by incubating
 PT immunogenic peptide(s) from antigen that binds class I major
 PT histocompatibility complex molecules with pre-treated antigen
 PT presenting cells

PS Example 4; Page 62; 104pp: English.

XX Sequences shown in AAW70010 to AAW70026 represent peptides derived from
 CC melanoma-associated antigen gp100 that can bind to a human leukocyte
 CC antigen (HLA), HLA-A2.1. The peptides are used to exemplify the method
 CC of invention of producing antigen-specific cytotoxic T cells (CTLs) in
 CC vitro. The method comprises contacting immunogenic peptides from an
 CC antigen that binds class I major histocompatibility complex (MHC)
 CC molecules with antigen presenting cells (APCs) pretreated with
 CC pretreatment growth factors, and incubating the APCs with purified CD8
 CC cells in the presence of at least 2 incubation growth factors, thereby
 CC producing antigen-specific CTLs. A method for specifically killing
 CC target cells in a human patient is also provided which comprises
 CC obtaining a fluid sample containing CTLs from a patient, contacting the
 CC cytotoxic T cells with APCs pretreated with pre-treatment growth
 CC factors, where the APCs comprise class I MHC molecules. The pretreated
 CC APCs are incubated with the cytotoxic growth factors, thereby producing
 CC activated CTLs which are contacted with a carrier to form a composition.
 CC The composition can then be administered to the patient. The activated
 CC CTLs can be used for treating cancers, immune disorders, viral
 CC infections, AIDS, hepatitis, bacterial infection, fungal infection,
 CC malaria or tuberculosis.

XX Sequence 9 AA:

Query Match 100.0%; Score 59; DB 19; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTWGQYMOV 9
 |||||
 Db 1 ktwgqyqv 9

RESULT 5

AAW54598
 ID AAW54598 standard; peptide; 9 AA.

AC AAW54598;

DT 25-SEP-1998 (first entry)

DE Peptide 3 from gp 100/Pmel-17.

XX Mannose; antigen; antigen-presenting cell; mannosylated peptide; T cell;
 KW vaccine; treatment.

OS Synthetic.

PN W09813378-A1.

PD 02-APR-1998.

PF 25-SEP-1997; 97WO-NL00536.

PR 26-SEP-1996; 96EP-0202701.

PA (UYLE-) RIJKSUNIV LEIDEN.

PI Drifhout JW, Konig F;

DR WPI; 1998-230631/20.

PT Increasing uptake and presentation of antigen(s) - by adding mannose
 PT residue(s) to antigen for increasing T cell response, useful in,
 PT e.g. vaccines against viral infection(s)

PS Disclosure; Page 24; 47pp: English.

XX The peptides AAW54598-W54809 are examples of peptides to which at least
 CC 1 (preferably 2) mannose can be attached to increase their uptake as
 CC antigens by antigen-presenting cells. Uptake of agonist mannosylated
 CC peptides will increase the T cell response, whereas uptake of antagonist
 CC peptides blocks the T cell response. Blocking binding of immunogenic
 CC autoantigens can be used in treatment of type I diabetes, rheumatoid
 CC arthritis, graft rejection etc., also to induce T-cell non-
 CC responsiveness. Vaccines containing mannosylated antigen are used to
 CC prevent or treat infections by, e.g. bacteria, viruses, fungi, helminths
 CC and parasites.

XX Sequence 9 AA:

Query Match 100.0%; Score 59; DB 19; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTWGQYMOV 9
 |||||
 Db 1 ktwgqyqv 9

RESULT 6

AAW5770
 ID AAW5770 standard; peptide; 9 AA.

AC AAW5770;

DT 22-JUN-1998 (first entry)

DE Melanoma associated peptide analogue #1.

KW Metastatic melanoma; peptide analogue; vaccine; cancer; diagnosis;
KM antigen; CTL; immunogenic; viral disease.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9802538-A1.
XX
PD 22-JAN-1998.
XX
PF 08-JUL-1997; 97WO-EP03712.
XX
PR 11-JUL-1996; 96EP-0201945.
XX
PA (ALKU) AKZO NOBEL NV.
XX
PI Adema GJ, Figdor CG;
XX
DR WPI; 1998-110586/10.
XX
PT Melanoma associated peptide analogues - useful in vaccines against
PT melanoma
XX
PS Claim 1; Figure 1; 47pp; English.
XX
CC This sequence represents a specifically claimed example of a novel
CC peptide, which is immunogenic with lymphocytes directed against
CC metastatic melanomas. It is characterised in that it comprises at least
CC a part of the following sequence, where the amino acid at position 2 or 8
CC is substituted: Lys-Thr-Trip-Gly-Gln-Tyr-Trip-Gln-Val. Vaccines comprising
CC the peptide, an epitope of the peptide, nucleotide sequence encoding the
CC peptide, or an antigen presenting cell preloaded with the peptide or
CC antibody, as above, are useful for cancer, particularly melanoma,
CC treatment. The peptides can also be used to generate antigen reactive
CC tumour infiltrating lymphocytes, which can also be used in vaccines. The
CC peptides can be exploited to elicit native epitope reactive CTL. Usage
CC of the peptides with improved immunogenicity may contribute to the
CC development of CTL-epitope based vaccines in viral disease and cancer.
CC
SQ Sequence 9 AA;

Query Match 100.0%; Score 59; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KTWGQYMOV 9
1 |||||||
Db 1 ktwgqyqwv 9

RESULT 7
AAV49663
ID AAV49663 standard; peptide; 9 AA.
XX
AC AAV49663;
XX
DT 14-JAN-2000 (first entry)
XX
DE Tumour antigenic peptide SEQ ID NO:30.
XX
KM Human; sdph3.10; SAGE; sdph3.8; HAGE; sdph3.5; TRAP; sarcoma;
KM tumour rejection antigen precursor; tumour associated nucleic acid;
KM carcinoma; cancer; immune response; diagnosis.
XX
OS Synthetic.
XX
PN WO9953061-A2.
XX
PD 21-OCT-1999.
XX
PF 14-APR-1999; 99WO-US08163.
XX

PR 15-APR-1998; 98US-0060706.
PR 27-JUL-1998; 98US-0122989.
PR 30-OCT-1998; 98US-0183706.
PR 30-OCT-1998; 98US-0183789.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Martelange V, De Smet C, Boon-Falleur T;
XX
DR WPI; 1999-620430/53.
XX
PT New nucleic acid encoding sarcoma-associated gene products, useful for
PT diagnosing, e.g. treating and preventing cancer
XX
PS Disclosure; Page 25; 93pp; English.
XX
CC The present invention describes sarcoma-associated gene products (I).
CC Agents, specifically sarcoma associated nucleic acids (II) or their
CC expression products that are tumour rejection antigens (TRA), that
CC selectively increase formation of HLA (human leucocyte antigen)/(I)
CC complexes are used for treating cancer, especially sarcoma and
CC carcinoma, in humans and other animals. Compositions containing
CC autologous cytolytic T cells (CTL), specific for the HLA/(I) complex,
CC are similarly useful, also transformed cells that stimulate such CTL
CC in vivo. (II) are also used; (I) as source of therapeutic antisense
CC sequences that reduce expression of (II); (II) for recombinant
CC production of (I); (III) particularly its fragments, as primers and
CC probes in usual hybridisation and amplification assays, for diagnosis,
CC prognosis and monitoring of tumours, or for measuring binding
CC specificity of HLA molecules or CTL clones; (IV) to identify related
CC sequences; and (V) for generating transgenic animals, e.g. for studying
CC cancer and immune responses to it. (I) are used to raise specific
CC antibodies (Ab) and therapeutically. Ab are used to diagnose tumours in
CC immunosays, also for delivering drugs, toxins, imaging agents etc. to
CC (I)-expressing cells. AAV49637 to AAV49670 represent exemplary tumour
CC antigenic peptides given in the present invention.
CC
SQ Sequence 9 AA;

Query Match 100.0%; Score 59; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KTWGQYMOV 9
1 |||||||
Db 1 ktwgqyqwv 9

RESULT 8
AAV53524
ID AAV53524 standard; Protein; 9 AA.
XX
AC AAV53524;
XX
DT 18-JAN-2000 (first entry)
XX
DE Human melanoma Pmel17 (gp100) (aa 154-162) binds HLA-A2.
XX
KM Lipopeptide; epitope; cytotoxic T lymphocyte; CTL; lipid; spacer; p53;
KM electrical charge; hydrophilicity; vaccine; immune response; HIV; HBV;
KM human immunodeficiency virus; hepatitis B virus; papilloma virus;
KM melanoma; malaria; parasite.
XX
OS Synthetic.
XX
PN FR2776926-A1.
XX
PD 08-OCT-1999.
XX
PF 07-APR-1998; 98FR-0004323.
XX

PR 07-APR-1998; 98FR-0004323.
XX
XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (CNRS) CNRS CENT NAT RECH SCI.
XX (INSP) INST PASTEUR LILLE.
XX
PI Le Gal FA, Gullet JG, Gahery SH, Gras MH, Melnyk O, Tartar A;
XX WPI; 1999-583113/50.
DR
XX
XX New lipopeptide containing lipid regions and two epitopes, all
PT separated by peptide spacers that impart hydrophilicity, useful in
PT vaccines
XX
XX
PS Disclosure; Page 24; 35pp; French.
XX
XX The invention relates to the generation of a lipopeptide comprising at
CC least one auxiliary T epitope, at least one cytotoxic T lymphocyte (CTL)
CC epitope and at least one lipid residue with (i) the epitopes and lipid
CC portion and (ii) the epitopes, being separated independently by peptide
CC spacers. These spacers comprise sequences of amino acids which carry an
CC overall electrical charge in neutral media to ensure that the
CC lipopeptide is hydrophilic. The peptides AAY3301-Y53549 represents
CC examples of peptide epitopes used to generate the lipopeptides. These are
CC used in therapeutic or prophylactic compositions and vaccines to induce
CC specific immune responses against human immunodeficiency, hepatitis B or
CC papilloma viruses; P53 of melanoma or the malaria parasite.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 59; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. NO. 3.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KTWGQYQV 9
Db 1 ktwgqyqv 9
|||||

RESULT 9
AAY47616
ID AAY47616 standard; Peptide; 9 AA.
XX
AC AAY47616;
XX
DT 01-DEC-1999 (first entry)
XX
DE Immunogenic peptide having a human leukocyte antigen binding motif #2227.
XX
KW Human leukocyte antigen: binding; immunogenic; glycoprotein; MHC; HLA;
KW immune response; T cell activation; major histocompatibility complex;
KW cytotoxic T lymphocyte; CTL; tumor rejection; viral infection; cancer;
KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
KW vaccine; immunisation.
XX
XX Synthetic.
OS Homo sapiens.
XX
PN WO9445954-A1.
XX
PD 16-SEP-1999.
XX
PF 13-MAR-1998; 98WO-US05039.
XX
PR 13-MAR-1998; 98WO-US05039.
XX
PA (EPIM-) EPIMUNE INC.
XX
PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
XX WPI; 1999-551214/46.
DR
XX

PT New immunogenic peptides with HLA binding motif, useful in treatment
PT and diagnosis of cancers and viral diseases
XX
XX Claim 1; Page 116; 150pp; English.
XX
CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
CC having a human major histocompatibility complex (MHC) Class I (also
CC known as human leukocyte antigen (HLA) binding motif. The immunogenic
CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
CC response against the antigen from which the peptide is derived.
CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
CC normally induced by an antigen in the form of a peptide fragment bound
CC to a HLA molecule, rather than the intact foreign antigen itself, and
CC are particularly important in tumour rejection and in fighting viral
CC infections. The peptides are therefore useful therapeutically to treat
CC or prevent viral infections and cancers in mammals (especially humans)
CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
CC They can be administered as vaccines to elicit an immune response in
CC individuals susceptible or otherwise at risk of viral infection or
CC cancer, or used to treat chronic or acute conditions. They are also
CC useful diagnostically, and can be used to induce a cytotoxic T cell
CC response, by contacting a cytotoxic T cell with the peptide e.g. to
CC produce CTLs ex vivo for infusion back into a patient. The
CC polynucleotides encoding the immunogenic peptides are also useful
CC therapeutically and for immunisation as above.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 59; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. NO. 3.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KTWGQYQV 9
Db 1 ktwgqyqv 9
|||||

RESULT 10
AAY33172
ID AAY33172 standard; peptide; 9 AA.
XX
AC AAY33172;
XX
DT 17-NOV-1999 (first entry)
XX
DE Human gp100-Pme1117 peptide #1.
XX
KW Human: protein delivery; Yersinia sp.; effector gene; mutant; antigen;
KW immune response; cytotoxic T-lymphocyte; CTL; vaccination; treatment;
KW pathological disorder; gp100-Pme1117.
XX
XX Homo sapiens.
OS
PN WO945098-A2.
XX
PD 10-SEP-1999.
XX
PF 03-MAR-1999; 99WO-IB00587.
XX
PR 06-MAR-1998; 98US-0036582.
XX
PA (VBRU/) VAN DER BRUGGEN P B.
PA (CORN/) CORNELIS G R.
PA (BOLA/) BOLAND A M.
PA (BOON/) BOON-FALEUR T R.
XX
PI Van Der Bruggen PB, Cornelis GR, Boland AM, Boon-Falleur TR;
XX WPI; 1999-540840/45.
DR
XX New mutant Yersinia strains useful for treating a pathological disorder
PT

Example 1 ; Page 71; 80pp; English.

This invention describes a novel mutant Yersinia (Y1) strain, comprising mutation(s) in effector-encoding gene(s) and deficient in the production of functional effector protein(s). The invention describes (1) a quadruple mutant Yersinia strain, having the designation Yersinia enterocolitica YOPEHOWP or Yersinia pseudotuberculosis YOPEHOWJ; (2) an expression vector (EV1) for delivering a heterologous protein into a eukaryotic cell, comprising in the 5'-3' direction; (3) a Yersinia or mutant Yersinia strain for delivering a heterologous protein into a eukaryotic cell, comprising contacting the cell with a Y1 transformed with the above vector (Y1-EV1); (4) a method for delivering a heterologous protein into a eukaryotic cell, comprising contacting the cell with a Y1 transformed with the above vector (Y1-EV1); (5) a method for inducing an immune response specific for a heterologous protein; (6) a method for inducing a cytotoxic T-lymphocyte (CTL) response specific for a heterologous protein; (7) a method for determining the efficacy of an antigen vaccination regimen in a subject. Y1 is used to treat a pathological disorder, by providing recombinant Yersinia for the safe delivery of proteins into eukaryotic cells. AAY31147-Y33178 are human-derived peptides used to illustrate the method of the invention.

Query Match	100.0%	Score 59;	DB 20;	Length 9;
Best Local Similarity	100.0%	Pred. No.	3.4e+05;	
Matches	9;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0

QY	1	KTWGQYQOV	9
Db	1	ktwgqyqv	9

RESULT	11
AA	AY40211
ID	AY40211 standard; Peptide; 9 AA

DT 19-NOV-1999 (first entry)

DE Amino acid sequence of a human melanoma epitope

KW Cytotoxic T cell; T lymphocyte; CD8+ epitope; T helper cell;

KW vaccine; tumor; immune response; cytokine profile;

KW autoimmune disease.

Homo sapiens.

PN FR2774687-A1.

PD 13-AUG-1999.

06-FEB-1998; 98FR-0001439.

06-FEB-1998: 98FEB-0001439

PA (INRM) INSERM INST NAT SANTE & RECH MEDICATE
AA

PA (INSP) INSP PASTEUR LILLE.
XX

PI THAM K, GUILLET JS, Ver waerde C, Auriault C, Gras MH, Loing E, XY

DR WPI; 1999-510734/43.

PT New lipopeptide comprising C-terminal interferon-gamma fragment with
PT attached lipophilic groups, used as interferon mimic, e.g. for treating
PT cancer or virus infection

PS Disclosure; Page 35; 53pp; French.

xx	AAV40123-740379 represent epitopes that are able to activate cytotoxic					
cc	T lymphocytes (CD8+ epitopes), T helper cells (CD4+ epitopes), or					
cc	B epitopes recognized by corresponding antibodies. The epitopes may be					
cc	used in the composition of the invention. The specification describes a					
cc	lipopeptide that has a peptide part derived from mammalian interferon					
cc	gamma (IFN γ) and one or more lipophilic parts comprising a linear or					
cc	branched, (unsaturated 4-20C hydrocarbon) chain or a steroid. The					
cc	lipopeptide mimics the activity of IFN γ . Compositions comprising the					
cc	lipopeptide are used to treat or prevent any condition that responds					
cc	to IFN γ , and as adjuvant for vaccines (particularly those directed					
cc	against tumors, viral or parasitic infections), to stimulate or					
cc	(re)orient the immune response between types 1 and 2 cytokine profiles.					
cc	Particular applications are treatment of infections (particularly					
cc	viral, e.g. acquired immune deficiency syndrome, papilloma (cancer) and					
cc	hepatitis, but also bacterial, fungal, parasitic or helminth); cancers					
cc	(particularly of kidney, cutaneous T cells or ovary, chronic					
cc	myelogenous leukemia or mesothelioma), allergy; and autoimmune					
cc	diseases.					
xx						
SQ	Sequence	9 AA;				
<hr/>						
	Query Match	100.0%;	Score 59;	DB 20;	Length 9;	
	Best Local Similarity	100.0%;	Pred. NO. 3.4e+05;			
Matches	9;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0	

Query Match	100.0%	Score 59;	DB 20;	length 9;
Best Local	Similarity 100.0%	Pred. No.	3 4e+05;	
Matches	9;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0

Qy	1	KTWGQYwQv	5
		1111111111	
Db	1	ktwgqywqv	5

```

RESULT 12
AAY26867
ID AAY26867 standard; peptide; 9 AA

```

AC AAY26867;

DT 14-SEP-1999 (first entry)

DE Melanoma-derived lipopeptide epitope #8 for mixed micelles.

KW Micelle; microaggregate; induction; immune response; lipopeptide; CTL;

KW tetanus; toxin; vaccine; HIV; hepatitis B virus; papilloma virus; p53;

XX
XX

syncretic.
Homo sapiens

AA
PN
FR2771640-A1

XX
PD 04-TTN-1999

XX 03-DEC-1997. 97FEB-0015246
DE

XX 03-DEC-1987. 02FB-0015346
 DP

XX
XX
CIVIL SERVICE NAME RECORD

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE

XX XX

PI Tartar A, Wieruszeski JM;

DR WPI; 1999-349509/30.

PT Immunogenic lipopeptide micelles - comprising lipopeptides

XX concentration of cocaine and heroin is improved in opiate

13 DISCLOSED, PAGE 31, VVPP, ETC.

cc The invention relates to the generation of mixed micelles of

CC microaggregates for inducing an immune response comprise: (a) a first
CC lipopeptide comprising at least one CTL (cytotoxic T-lymphocyte) epitope
CC and at least one lipid unit; and (b) a second lipopeptide comprising at
CC least one HTL (helper T-lymphocyte) epitope and at least one lipid unit
CC different from that of the first lipopeptide. This peptide represents
CC an example of a lipopeptide epitope used in the invention and is derived
CC from a human melanoma protein. The immunogenic lipopeptide micelles
CC are used in vaccines, especially against HIV, hepatitis B virus (HBV),
CC papilloma viruses, p53, melanoma or Plasmodium falciparum malaria.

XX Sequence 9 AA:

Query Match 100.0%; Score 59; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTWGYQWQV 9
Db 1 ktwgqyqwv 9

RESULT 13
AA01753 standard; Peptide: 9 AA.

AC AA01753;

DT 25-JUN-1999 (first entry)

DE Exemplary antigenic peptide derived from gp100(Pmel117).

KW MAGE-3; tumour associated gene; human leucocyte antigen Class II;

KW autologous CD4+ cell; MAGE-3 related disease; cancer; melanoma;
KM osteosarcoma; leukemia; carcinoma.

XX Homo sapiens.

PN WO914326-A1.

PD 25-MAR-1999.

PF 04-SEP-1998; 98WO-US18601.

PR 12-SEP-1997; 97US-0928615.

PA (LUDW-) LUDWIG INST CANCER RES.

PA (UYVR-) UNIV VIRJE BRUSSEL.

PI Boon-Falleur T, Chaux P, Cortals J, Heirman C;
PI Luiten R, Stroobant V, Thielemans K, Van Der Bruggen P;

DR WPI: 1999-244031/20.

PT Isolated peptides that bind to human leucocyte antigen class II

PT molecules

PS Disclosure: Page 29; 88pp; English.

CC The present sequence represents an exemplary tumour associated peptide
CC antigen. The specification describes a MAGE-3 tumour associated gene.
CC Peptides (AA01721-25) that bind human leucocyte antigen (HLA) Class II
CC molecules can be derived from the MAGE-3 protein. These peptides and
CC autologous CD4+ cells that bind to a complex of MAGE-3 peptide
CC and HLA Class II, are used to treat MAGE-3 related diseases,
CC particularly cancers (e.g. melanoma, osteosarcoma, leukemia and
CC various forms of carcinoma). The peptides are also used to produce
CC specific antibodies. Detection of the peptides, e.g. in binding
CC assays, particularly with antibodies, is used for diagnosis of such
CC diseases.

XX Sequence 9 AA:

Query Match 100.0%; Score 59; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTWGYQWQV 9
Db 1 ktwgqyqwv 9

RESULT 14
AA00715 standard; peptide: 9 AA.

AC AA00715;

DT 12-MAY-1999 (first entry)

DE Tumour antigen booster peptide gp100Pmel117 HLA-A2 #1.

KW Tumour antigen; booster peptide; immune response modulation; allergy;

KW immune response enhancer; tumour cell; tumour rejection antigen;

KW leukocyte antigen-presenting molecule; autoimmune disease;
KW allograft rejection.

XX Homo sapiens.

PN WO9858956-A2.

PD 30-DEC-1998.

PF 19-JUN-1998; 98WO-US12894.

PR 23-JUN-1997; 97US-0880979.

PA (LUDW-) LUDWIG INST CANCER RES.

PI Boon-Falleur T, Uytendhoe C, Warnier G;

DR WPI: 1999-105612/09.

PT Immunization methods using viruses expressing antigen for priming
PT and booster immunizations - useful for modulating immune responses
PT against antigen, e.g. enhancing immune response against tumour cells
PT expressing tumour rejection antigens

PS Disclosure: Page 10; 33pp; English.

CC This sequence represents a tumour antigen booster peptide that can be
CC used in the method of the invention. The method is for modulating an
CC immune response in a mammal against an antigen, and comprises:
CC (A) inducing an immune response by: (i) administering a virus containing
CC a nucleic acid molecule encoding the antigen or its precursor to generate
CC an immune response; and (ii) administering at least one booster dose
CC comprising a peptide including the antigen, in an adjuvant, in a combined
CC amount effective to enhance the initial immune response; or
CC (B) reducing an immune response as defined for (A) but using a
CC non-adjuvant with the peptide which includes the antigen, in an amount
CC effective to reduce the initial immune response. Method (A) is used to
CC enhance the immune response against tumour cells expressing tumour
CC rejection antigens, and against pathogens in subjects having human
CC leukocyte antigen-presenting molecules. Method (B) is used to reduce the
CC immune response in allergy, autoimmune disease, and allograft rejection.
CC Method (A) provides an immunisation method which, unlike prior art, is
CC not limited by the host immune response against viral vectors.

XX Sequence 9 AA:

Query Match 100.0%; Score 59; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KTWGQYQV 9
 ID |||||
 DB 1 ktwgqyqv 9

RESULT 15

AAI0449 standard; Peptide; 9 AA.

AC AAI0449;

DT 12-MAY-1999 (first entry)

DE HLA Class I motif peptide SEQ ID NO:379.

KW Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system;
 immunisation; tumour; infectious disease; immunotherapy; cancer;
 malignant melanoma; viral disease; hepatitis; AIDS.

OS Synthetic.

OS Homo sapiens.

PN MO9902183-A2.

PD 21-JAN-1999.

PF 10-JUL-1998; 98WO-US14289.

PR 10-DEC-1997; 97US-0988320.

PR 10-JUL-1997; 97CA-2209815.

PA (CTL-) CTL IMMUNOTHERAPIES CORP.

PI Kuendig TM, Simard JLL;

DR WPI: 1999-120514/10.

PT Inducing a cytotoxic T lymphocyte response - by maintaining a level
 of antigen in the lymphatic system of a mammal so as to provide a
 sustained CTL response, used to treat, e.g. AIDS

PS Disclosure; Page 40; 1999p; English.

CC The present invention describes a method of inducing and/or sustaining
 an immunological cytotoxic T lymphocyte (CTL) response in a mammal. The
 method comprises: (a) delivering an antigen to the mammal at a level to
 induce an immunological CTL response in the mammal; and (b) maintaining
 the level of the antigen in the mammal's lymphatic system to maintain
 the immunologic CTL response. The method can be used for the delivery of
 e.g. a differentiation antigen, a tumour-specific multilinage antigen,
 an embryonic antigen, an oncogene antigen, a mutated tumour-suppressor
 gene antigen, or a viral antigen. They can be used for the treatment of
 disease such as cancer, e.g. malignant melanoma or infectious disease,
 e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery
 to the lymphatic system provides for potent CTL stimulation that takes
 place in the milieu of the lymphoid organ, and it sustains stimulation
 that is necessary to keep CTL active, cytotoxic and recirculating
 through the body. AAI0071 to AAI0639 represent examples of peptide
 antigens given in the present invention.

CC Sequence 9 AA;

Query Match 100.0%; Score 59; DB 20; Length 9;

Best Local Similarity 100.0%; Pred. No. 3.4e+05; Mismatches 0; Indels 0; Gaps 0;

OY 1 KTWGQYQV 9
 ID |||||
 DB 1 ktwgqyqv 9

RESULT 16

AAB33662
 ID AAB33662 standard; Peptide; 9 AA.

AC AAB33662;

DT 26-JAN-2001 (first entry)

DE MHC class I associated immunogenic peptide SEQ ID 61.

KW Microparticle; nucleic acid delivery; immunogenic peptide; MHC I; MHC II;
 major histocompatibility complex; vaginal tissue; mucosal tissue..

OS Unidentified.

PN WO200053161-A2.

PD 14-SEP-2000.

PF 10-MAR-2000; 2000WO-US06578.

PR 11-MAR-1999; 99US-0266463.

PR 27-MAY-1999; 99US-0321346.

PA (ZYCO-) ZYCO INC.

PI Lunsford IB, Putnam D, Hedley ML;

DR WPI: 2000-638130/61.

PT Microparticles useful for administering a nucleic acid into the mucosal
 tissue preferably vaginal tissue of an animal, comprises a polymeric
 matrix, a lipid and a nucleic acid molecule

PS Disclosure; Page 14; 96pp; English.

CC The present invention relates to microparticles which are less than 20
 microns in diameter, which comprise a polymeric matrix, a lipid and a
 nucleic acid molecule. The microparticle is specifically not
 encapsulated in a liposome and does not comprise a cell. The nucleotide
 sequence encodes an expression product that binds to major
 histocompatibility complex (MHC) type I or II molecules. Peptides
 AAB33602-B33647 represent MHC class II associated immunogenic peptides,
 and AAB33648-B33710 represent MHC class I associated immunogenic
 peptides. The peptides are examples of the expression products of the
 nucleotide sequences which can be included in the microparticles of the
 invention. Sequences AAB33711-B33716 represent alternative expression
 products and nuclear localisation signals also used in the invention. The
 microparticles are useful for administering a nucleic acid into the
 mucosal tissue preferably vaginal tissue of an animal.

CC Sequence 9 AA;

Query Match 100.0%; Score 59; DB 21; Length 9;

Best Local Similarity 100.0%; Pred. No. 3.4e+05; Mismatches 0; Indels 0; Gaps 0;

OY 1 KTWGQYQV 9
 ID |||||
 DB 1 ktwgqyqv 9

RESULT 17

AAB23679
 ID AAB23679 standard; Peptide; 9 AA.

AC AAB23679;

DT 05-JAN-2001 (first entry)

DE Cytotoxic T lymphocyte (CTL) epitope SEQ ID NO:31.

KW ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;

KW Immune response; infectious disease; malaria; cytotoxic T cell;
KW cytostatic; immunostimulant; cellular immune response inducer;
KW protozoacide; leukaemia; cancer.
XX
OS Homo sapiens.
PN WO200049041-A1.
XX
PD 24-AUG-2000.
XX
PF 18-FEB-2000; 2000WO-JP00941.
XX
PR 19-FEB-1999; 99JP-0041535.
XX
PA (SUME) SUMITOMO ELECTRIC IND CO.
XX
PI Shinbara N, Udono H, Yui K;
XX
DR WPI; 2000-543748/49.
XX
PT Fused protein capable of inducing cellular immune response, useful as
PT active ingredient for drug compositions in preventing and/or treating
PT infectious diseases such as malaria or cancer
XX
PS Claim 7; Page 58; 72pp; Japanese.
XX
CC The present invention describes a fused protein (I) prepared from a
CC peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by
CC cytotoxic T cells and a protein containing the ATPase domain of a heat
CC shock protein. Also described are: (1) a drug composition containing (I)
CC as active ingredient; (2) a DNA encoding (I); (3) an expression vector
CC containing the DNA of (2); and (4) a transformant which can retain the
CC expression vector of (3). (I) has cytostatic, immunostimulant and
CC protozoacide activities, and can be used as a cellular immune response
CC inducer. The protein is useful as an active ingredient for drug
CC compositions in preventing and/or treating infectious diseases such as
CC malaria or cancer e.g. to provide systemic immunity against leukaemia.
CC The present sequence represents a specifically claimed CTL epitope
CC for use in a fused protein of the present invention.
XX
SQ Sequence 9 AA:

Query Match 100.0%; Score 59; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTWGQYQV 9
Db 1 ktwgqyqv 9
|||||
1 ktwgqyqv 9

RESULT 18
AAB08694
ID AAB08694 standard; Peptide: 9 AA.
XX
AC AAB08694;
XX
DT 02-JAN-2001 (first entry)
XX
DE Antigenic peptide from tumour rejection antigen gp100(Pmel117).
XX
KW Epha3; HLA class II-binding peptide; human leukocyte antigen; antigen;
KW CD4+ T lymphocyte; tumour associated gene; vaccine.
XX
OS Homo sapiens.
XX
PN WO200050589-A1.
XX
PD 31-AUG-2000.
XX
PF 18-FEB-2000; 2000WO-US04326.
XX

PR 22-FEB-1999; 99US-0121170.
PR 08-OCT-1999; 99US-0158566.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Chari R, Coulie P, Boon-Falleur T;
XX
DR WPI; 2000-572089/53.
XX
XX Novel tyrosine kinase receptor, Epha3 human leukocyte antigen (HLA)
PT class II binding peptide and nucleic acid encoding the receptor, useful
PT for diagnosing and treating conditions characterized by expression of
PT Epha3 gene
XX
PS Disclosure; Page 35; 107pp; English.
XX
XX AAB08668-B08704 represent antigenic peptides characteristic of tumours.
CC The peptides may be combined in vaccines with a human Epha3 HLA (human
CC leukocyte antigen) class II-binding peptide. Epha3 antigens, when
CC presented by an antigen presenting cell having a HLA class II molecule,
CC effectively induce activation and proliferation of CD4+ T lymphocytes.
CC Epha3 is a tumour associated gene. Epha3 HLA binding peptides are used
CC for selectively enriching a population of T lymphocytes. The peptides
CC are also used for diagnosing a disorder characterized by Epha3 or Epha3
CC HLA binding peptide expression. The peptides are also used to treat a
CC disorder characterized by Epha3 expression. The Epha3 binding peptides
CC are useful in producing vaccines and antibody.
XX
SQ Sequence 9 AA:

Query Match 100.0%; Score 59; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTWGQYQV 9
Db 1 ktwgqyqv 9
|||||
1 ktwgqyqv 9

RESULT 19
AAV71520
ID AAV71520 standard; peptide: 9 AA.
XX
AC AAV71520;
XX
DT 12-OCT-2000 (first entry)
XX
DE Human gp100 Pmel117 nonapeptide-1.
XX
KW gp100 Pmel117; human; Tumour Rejection Antigen; TRA; tumour; cancer;
KW HLA; Human Leucocyte Antigen; MHC; Major Histocompatibility Complex; CTL;
KW cytolytic T-lymphocyte; immune response stimulator; prophylaxis; therapy;
KW diagnosis; TNF; tumour necrosis factor; vaccine; cytostatic.
XX
OS Homo sapiens.
XX
PN WO200032769-A2.
XX
PD 08-JUN-2000.
XX
PF 26-NOV-1999; 99WO-IB02018.
XX
PR 27-NOV-1998; 98GB-0026143.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Huang L, Van Pel A, Brasseur F, De Plaen E, Boon T;
XX
DR WPI; 2000-412317/35.
XX
PT Novel polypeptides expressed in tumor cells useful for treating cancers
PT have an ability to complex with a major histocompatibility complex

PT molecule and comprises a specific unbroken amino acid sequence
 XX
 PS Disclosure: Page 20; 80pp; English.
 XX
 CC The patent discloses MAGE-A10 and MAGE-A8 polypeptide, nonapeptide and
 CC decapeptide sequences, that function as tumour rejection antigens
 CC (TRAs). These peptides are capable of forming a complex with major
 CC histocompatibility complex (MHC) molecule type HLA-A2.1 (Human Leucocyte
 CC Antigen), that are recognised by T-lymphocytes and elicit an immune
 CC response from cytolytic T-lymphocytes (CTL). They function as an immune
 CC response stimulator. Tumour rejection antigens are useful in prophylaxis,
 CC therapy and diagnosis of tumours and are effective in controlling or
 CC preventing tumour growth. The present sequence is the human gp100 Pmel17
 CC nonapeptide-1, that corresponds to residues 154-162 of the tumour
 CC associated gene, gp100 Pmel17 encoding protein. It can be administered
 CC to induce or enhance an immune response and is presented by HLA-A2
 CC complex. This peptide can serve as a tumour rejection antigen (TRA) and
 CC in combination with adjuvants, can produce vaccines useful for treating
 CC a variety of tumours.
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 59; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KTWGQYMOV 9
 |||||
 DB 1 ktwgqymv 9

RESULT 20

AAB02622
 ID AAB02622 standard; Peptide; 9 AA.

AC AAB02622;

DT 18-AUG-2000 (first entry)

XX Tumour associated peptide antigen from gp100 #2.

XX MAGE-A3; HLA class II; human leukocyte antigen; antibody; vaccine;
 KM cancer; human; tumour; tumour associated gene product.

OS Homo sapiens.

PN WO200020581-A1.

PD 13-APR-2000.

PF 15-SEP-1999; 99WO-US21230.

PR 05-OCT-1998; 98US-0166448.

PA (LUDM-) LUDMIG INST CANCER RES.

PA (UYVR-) UNIV YRIE BRUSSEL.

PI Chaux P, Stroobant V, Boon-Falleur T, Van Der Bruggen P;
 PI Schultz ES, Van Snick J, Lethe B, Thielemans K, Cortals J;
 PI Heitman C;

XX WPI: 2000-317713/27.

PT New MAGE-A3 class II binding peptides, useful to diagnose and treat
 PT tumours, are fragments of MAGE-A3 which bind to and are presented to T
 PT lymphocytes by human leukocyte antigen class II molecules
 XX
 XX Disclosure: Page 33; 119pp; English.

XX The present invention relates to MAGE-A3 (tumour associated gene
 CC product) human leukocyte antigen (HLA) class II-binding peptides (see
 CC AAB02566-B02565, and AAB02633-B02637). These peptides are presented to T

CC cells in the context of HLA class II molecules. The peptides stimulate
 CC the activity and proliferation of CD4+ T lymphocytes. The invention also
 CC includes nucleotide sequences encoding MAGE-3A peptides (see AAA37928
 CC and AAA37938-A37940). The peptides and nucleotide sequences can be used
 CC to create antibodies against the MAGE-A3 peptides, the antibodies, the
 CC peptides and nucleotide sequences can be used to create a vaccine. The
 CC peptides are used to diagnose or treat a disorder characterized by
 CC expression of MAGE-3, particularly cancer. The methods can also be used
 CC in the diagnosis of disorders associated with MAGE-3 expression. Included
 CC in the invention are other human tumour antigens (see AAB02596-B02637),
 CC and PCR primers used in the course of the invention (see AAA37929-A37937
 CC and AAA37941-A37942).
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 59; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KTWGQYMOV 9
 |||||
 DB 1 ktwgqymv 9

RESULT 21

AA90803
 ID AA90803 standard; peptide; 9 AA.

AC AA90803;

DT 25-AUG-2000 (first entry)

XX Human leukocyte antigen A2 gp100-Pmel17 peptide SEQ ID NO:32.

XX Human leukocyte antigen; HLA-B35; binding; recognition; lysis;
 KM cytolytic T cell; tyrosinase; immune response; diagnosis;
 KM identification; human.

XX Homo sapiens.

OS Homo sapiens.

PN WO200021551-A1.

PD 20-APR-2000.

PF 04-OCT-1999; 99WO-US23038.

PR 09-OCT-1998; 98US-0169717.

PA (LUDM-) LUDMIG INST CANCER RES.

PA Ooms A, De Giovanni G, Morel S, Van Den Eynde B, Boon-Falleur T;

DR WPI: 2000-317842/27.

PT Isolated peptides, sometimes derived from tyrosinase, which bind to
 PT HLA-B35 leading to recognition and lysis of the resulting complexes by
 PT cytolytic T cells
 XX
 XX Example 3; Page 9; 20pp; English.

XX The present invention describes isolated peptides which bind to human
 CC leukocyte antigen (HLA)-B35 molecules leading to recognition and lysis
 CC of the resulting complexes by cytolytic T cells. The isolated peptides
 CC are sometimes derived from tyrosinase. Compositions comprising the
 CC peptides of the invention can be used to generate immune responses,
 CC preferably in humans, but also in non-human animals to generate immune
 CC components which can then be used to treat humans or diagnostically.
 CC Therapeutically, the peptides are useful in generation of cytolytic T
 CC cells either in vitro or in vivo which specifically lyse pathogenic
 CC cells. The peptides can also be used to identify HLA-B35 positive
 CC cells, or to remove HLA-B35 positive cells from mixtures containing
 CC such cells. Nucleic acid molecules encoding the peptides can be used

CC Inter alia as probes to identify cells which are expressing tyrosinase.
 CC The present sequence represents an HLA binding peptide used in the
 CC exemplification of the present invention.

XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 59; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KTWGQYMOV 9
 1 ktwgqywgqv 9

RESULT 22

AAV92299
 ID AAV92299 standard; peptide; 9 AA.

XX
 AC AAV92299;

DT 10-AUG-2000 (first entry)

XX gp100-Pmel117 antigenic peptide epitope (residues 154-162).

XX gp100-Pmel117; antigen; epitope; cytotoxic T lymphocyte; CTL; complex;

KW human leukocyte antigen; HLA.

XX Homo sapiens.

XX WO200020445-A2.

XX 13-APR-2000.

XX 15-SEP-1999; 99WO-IB01664.

XX 02-OCT-1998; 98US-0165863.

XX 09-APR-1999; 99US-0289350.

XX (CHAU/) CHAUX P.

XX (LUIT/) LUITEN R.

XX (DEMO/) DEMOTE N.

XX (DUFF/) DUFFOUR M.

XX (LURQ/) LURQUIN C.

XX (TRAY/) TRAVERSARI C.

XX (STRO/) STROOBANT V.

XX (CORN/) CORNELIS G R.

XX (BOON/) BOON-FALLEUR T.

XX (YBRU/) VAN DER BRUGGEN P.

XX

XX

XX

XX

XX

XX

CC A novel method of isolation of cytotoxic T-lymphocytes (CTL) clones
 CC comprises successive steps of stimulation and testing of lymphocytes
 CC with antigen presenting cells (APCs) which present antigens derived
 CC from different expression systems. The CTL clones isolated recognize
 CC specific antigenic peptides of proteins, preferably of the MAGE family.
 CC The APC is autologous and each expression system is different from at
 CC least one of the other expression systems, therefore isolating a
 CC cytotoxic T cell clone specific for the protein. The method can also be
 CC used to identify an antigenic peptide epitope. Isolated CTL clones
 CC specific for a peptide/human leukocyte antigen (HLA) complex are claimed.

CC The CTL cells specific for the complexes, peptides or cells which present
 CC the complexes on the cell surface are useful for treating pathological
 CC conditions characterized by abnormal expression of the complexes.

XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 59; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KTWGQYMOV 9
 1 ktwgqywgqv 9

RESULT 23

AAV84296
 ID AAV84296 standard; peptide; 9 AA.

XX
 AC AAV84296;

DT 12-JUL-2000 (first entry)

XX Tumour associated antigen derived from gp100-Pmel117.

XX tumour rejection antigen; macrophage colony stimulating gene;

KW macrophage-colony stimulating factor; antigen presenting cell;

XX human leukocyte antigen; CD8+ cytotoxic T lymphocyte.

XX Homo sapiens.

XX WO200013699-A1.

XX 16-MAR-2000.

XX 03-SEP-1999; 99WO-US20344.

XX 04-SEP-1998; 98US-0099077.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Probst-Keeper M, Van Den Eynde B, Boon-Falleur T;

XX WPI: 2000-256859/22.

XX Isolated polypeptide used to treat subjects having a disorder

XX characterized by expression of alternative open reading frame

XX macrophage-colony stimulating factor comprises 25 amino acid residue

XX sequence -

XX Disclosure; Page 21; 74pp; English.

XX AAV84270-Y84303 represent peptides which are tumour associated antigens.

XX They can be administered in conjunction with the tumour rejection antigen

XX precursor of the invention to induce anti-tumour responses. The tumour

XX rejection antigen precursor of the invention is encoded by an

XX alternative open reading frame (ORF) of human macrophage colony

XX stimulating gene. Peptides derived from the alternative ORF of

XX macrophage-colony stimulating factor, when presented by an antigen

XX presenting cell having a human leukocyte antigen (HLA) class I molecule,

XX effectively induce the activation and proliferation of CD8+ cytotoxic T

XX lymphocytes. Polypeptide and nucleic acids derived from the alternate ORF

XX of macrophage-colony stimulating factor are useful for enriching

XX selectively a population of T lymphocytes with CD8+ T lymphocytes. They

XX are also useful for diagnosing a disorder characterized by expression of

XX the polypeptide, and for identifying functional variants and mimetics.

XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 59; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTMGOYMOV 9
| | | | | | | | | |
Db 1 KTMGYWYV 9

RESULT 24
AAV82979
ID AAV82979 standard; Peptide; 9 AA.

AC AAV82979;

DF 19-JUN-2000 (first entry)

DE gp100(Pmel117) tumour associated antigen.

KM Tumour; tumour associated antigen; retrovirus; antisense;
KW treatment; probe; primer; HLA; cytotoxic T-lymphocyte; cancer;
KW testis; antibody; CTL; helper T-lymphocyte; MAGE; BAGE; RAGE;
KW Gnt-V; MUM; CDK4; beta catenin; tyrosinase; Melan-A; gp100; PRAME.

OS Homo sapiens.

PN WO200006598-A1.

PD 10-FEB-2000.

PF 15-JUL-1999; 99WO-US16236.

PR 29-JUL-1998; 98US-0124398.

PA (LUDM-) LUDMIG INST CANCER RES.

PI Coulie P, Boon-falleur T;

DR WPI: 2000-205453/18.

XX Novel nucleic acids encoding melanoma associated gene products and
PT their fragments and variants, useful for treating endogenous retrovirus
PT mediated tumors, especially melanomas

PS Disclosure; Page 26; 77pp; English.

CC Tumors associated disorders (e.g. endogenous retrovirus mediated
CC tumors, especially melanomas) can be treated or ameliorated by
CC administering antisense nucleic acid to reduce the expression of
CC tumor associated genes such as HERV-AVL3-B. Progression of
CC a disorder characterized by the expression of the HERV-AVL3-B
CC endogenous retrovirus tumor rejection antigen (EVRPA) can be
CC diagnosed or monitored by contacting a non-testis biological
CC sample with an agent that binds to the complex and determining
CC the interaction. A disorder can also be treated by administering
CC an agent that enriches the presence of HLA and HERV-AVL3-B EVRPA
CC or by administering autologous cytotoxic T-cells sufficient to
CC ameliorate the disorder. Fragments of the HERV-AVL3-B coding sequence
CC are useful as probes or amplification primers for determining the
CC expression of HERV-AVL3-B genes, to express tumor associated
CC polypeptides in vivo and in vitro and to prepare fragments of such
CC polypeptides to synthesize antibodies. Antigenic peptides of
CC HERV-AVL3-B can be useful for generating antibodies either alone or
CC as fusion proteins, as components of immunoassay and for determining
CC the binding specificity of HLA molecules and/or cytotoxic T
CC lymphocyte (CTL) for HERV-AVL3-B proteins. Peptides derived from
CC the HERV-AVL3-B coding sequence and which are presented by MHC
CC molecules and recognised by CTL or helper T-lymphocytes can be
CC combined with peptides from other tumour rejection antigens by
CC preparation of hybrid nucleic acids or polypeptides to produce
CC polytopes. This exemplary tumour associated peptide antigen
CC corresponds to amino acids 154-162 of the gp100(Pmel117) polypeptide.
CC See also AAV82953-Y82986.

XX Sequence 9 AA;

Query Match 100.0%; Score 59; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTMGOYMOV 9
| | | | | | | | | |
Db 1 KTMGYWYV 9

RESULT 25
AAV56614

ID AAV56614 standard; peptide; 9 AA.

AC AAV56614;

DF 21-FEB-2000 (first entry)

DE gp100-Pmel-117 gene MHC molecule HLA-A2 peptide SEQ ID NO:30.

KM HLA-A*0201; human leukocyte antigen; cytolytic T cell; CTL; tumour;
KW Melan-A; peripheral blood lymphocyte; FBL; immune complex; melanoma;
KW MHC molecule; beta2-microglobulin; cytotoxic T lymphocyte; vaccine;
KW immune response; cancer; tyrosinase; tumour rejection antigen;
KW major histocompatibility complex.

OS Synthetic.

OS Homo sapiens.

PN WO9950637-A2.

PD 07-OCT-1999.

PF 25-MAR-1999; 99WO-US06615.

PR 27-MAR-1998; 98US-0049850.

PA (LUDM-) LUDMIG INST CANCER RES.

PI (UYOX-) UNIV OXFORD.

DR Romero P, Dunbar R, Valmori D, Ogg G, Cerrotini J, Cerundolo V;

XX WPI: 2000-052636/04.

XX New isolated complex of binding partners and immune complexes
PT containing major histocompatibility molecules and peptide, used to
PT isolate and detect cytotoxic T cells, particularly directed against
PT cancer

PS Example 50; Page 64; 91pp; English.

CC The present invention describes an isolated complex (A) comprising: (1)
CC first and second binding partners (BP1, BP2); and (11) several immune
CC complexes (IC) containing a major histocompatibility complex (MHC)
CC molecule (I), a beta2-microglobulin molecule (b2Mc) and a peptide (II)
CC that binds specifically to (I). (A) are used for analysis of cytolytic
CC T cells (CTL) for characterisation of an immune response to tumours or
CC for monitoring vaccine trials. Particularly they are used to isolate or
CC detect particular CTL (especially those in tumour-infiltrated lymph
CC nodes), including visualisation of antigen-specific CTL and determination
CC if the cells have been activated by in vivo exposure to antigen. Isolated
CC precursor cells may be expanded in vitro to produce cells with high
CC tumoricidal activity, for therapeutic or diagnostic use. A method from
CC the present invention allows: (1) preselection of T cell clones for use
CC in immunotherapy according to their homing molecules; and (11) improves
CC the lytic activity of T cells populations by inhibition of natural
CC killer cell receptors. The present sequence represents a peptide
CC used in the exemplification of the present invention.

XX Sequence 9 AA;

Query Match 100.0%; Score 59; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KTWGQYMOV 9
 |||||||
 1 ktwgqyqgv 9

RESULT 26

AAB31354
 ID AAB31354 standard; peptide; 9 AA.

XX AAB31354;

XX 20-APR-2001 (first entry)

XX Exemplary antigen characteristic of tumours, derived from gp100.

XX MAGE-A1: HLA: human leukocyte antigen; CD4+ T lymphocyte; cancer;

KW MAGE-A1 HLA class II-binding protein; vaccine.

XX Homo sapiens.

XX WO200078806-A1.

XX 28-DEC-2000.

XX 14-JUN-2000; 2000WO-US16287.

XX 18-JUN-1999; 99US-0336091.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Van Snick J, Lethe B, Chaux P, Boon-Fallier T, Van Der Bruggen P;

XX WPI: 2001-102698/11.

XX Novel MAGE-A1 human leukocyte antigen class II peptides which bind to
 PT and are presented to the class II molecules, useful for inducing immune
 PT response and treating cancers characterized by expression of MAGE-A1 -

XX Disclosure; Page 33; 78pp; English.

XX AAB31302-59 represent exemplary antigens which are characteristic
 CC of tumours. They can be used to enhance the immune response of vaccines
 CC comprising peptides derived from human MAGE-A1 HLA (human leukocyte
 CC antigen) class II-binding protein. Peptides derived from the MAGE-A1 HLA
 CC binding protein stimulate the activity and proliferation of CD4+ T
 CC lymphocytes. The MAGE-A1 HLA binding protein is useful as a diagnostic
 CC agent for diagnosing a disorder characterized by expression of MAGE-A1.
 CC The protein is used for treating a disorder characterized by expression
 CC of MAGE-A1 such as cancers e.g. melanoma, squamous cell carcinomas,
 CC colorectal carcinomas, osteosarcomas, and lymphocytic leukemias.
 CC Peptides derived from the MAGE-A1 HLA binding protein are useful in the
 CC production of anti-tumour vaccines.

XX Sequence 9 AA:

Query Match 100.0%; Score 59; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KTWGQYMOV 9
 |||||||
 1 ktwgqyqgv 9

RESULT 27

AAR78643
 ID AAR78643 standard; Protein; 10 AA.

AC AAR78643;

XX 22-JAN-1996 (first entry)

XX Immunogenic peptide of melanoma associated antigen gp100.

KW Melanoma; antigen; vaccine; immunogen; primer; probe; detection;

KW Identification; tumour; gp100.

XX Homo sapiens.

XX EP668350-A1.

XX 23-AUG-1995.

XX 14-FEB-1995; 95EP-0200348.

XX 21-DEC-1994; 94EP-0203709.

XX 16-FEB-1994; 94EP-0200337.

PA (ALKU) AKZO NOBEL NV.

XX Adema GJ, Figdor CG;

XX WPI: 1995-284790/38.

XX N-PSDB; AAQ96055.

XX Melanoma associated antigen gp100 - used in vaccines and for the
 PT detection of tumours

XX Claim 5; Page 31; 40pp; English.

XX Immunogenic peptides derived from the melanoma associated antigen
 CC (see AAR78639-45) may be used in the production of vaccines.
 CC Nucleotide sequences encoding the immunogenic peptides may be used
 CC as primers and probes in the detection of melanoma cells. Tumour
 CC infiltrating lymphocytes capable of binding to the melanoma
 CC associated antigen can be cultured ex vivo and returned to melanoma
 CC particles, and when radiolabelled, they may be used to identify
 CC tumour deposits.

XX Sequence 10 AA;

Query Match 100.0%; Score 59; DB 16; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0024;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KTWGQYMOV 9
 |||||||
 1 ktwgqyqgv 9

RESULT 28

AAR84209
 ID AAR84209 standard; Peptide; 10 AA.

XX AAR84209;

XX 25-APR-1996 (first entry)

XX gp100 melanoma antigen immunogenic peptide (G10-154).

KW gp100; melanoma antigen recognised by T-cells; MART; melanoma;

KW metastatic melanoma; tumour-associated antigen;

KW immunogenic peptide; diagnosis; prognosis; prophylaxis;
 KW therapy; vaccine.

XX Synthetic.

XX WO9529193-A2.

XX 02-NOV-1995.

XX 21-APR-1995; 95WO-US05063.
XX
XX 05-APR-1995; 95US-0417174.
PR 22-APR-1994; 94US-0231565.
XX
XX (USSH) US SEC DEPT HEALTH.
PA
XX Kawakami Y, Rosenberg SA;
PI
XX WPI, 1995-382963/49.
DR
XX
XX DNA encoding melanoma antigens recognised by T-lymphocytes - also
PT vectors, host cells and antibodies, used to detect, treat and
PT immunise animal against melanoma.
XX
XX Claim 55; Page 131; 184pp; English.
PS
XX The immunogenic peptide is derived from CDNA25 (AAR84854), a
CC melanoma antigen derivative of gp100 (see AAR84855). The
CC peptide and its derivatives (see AAR84200-R84211) are used in
CC medicaments (vaccines) for the treatment or prevention (by
CC immunization) of melanoma. Antibodies against melanoma-specific
CC antigens and its immunogenic peptides may be used in the
CC detection and isolation of the antigen from a sample, the
CC detection of which is indicative of a disease state
CC (melanoma or metastatic melanoma).
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 59; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTWGQYWCY 9
| | | | | | | | | |
DB 1 KTWGQYWCY 9

RESULT 29
AAR78642
ID AAR78642 standard; Protein; 11 AA.
XX
AC AAR78642;
XX
DT 22-JAN-1996 (first entry)
XX
DE Immunogenic peptide of melanoma associated antigen gp100.
XX
XX Melanoma; antigen; vaccine; immunogen; primer; probe; detection;
KW identification; tumour; gp100.
XX
OS Homo sapiens.
XX
PN EP668350-A1.
XX
PD 23-AUG-1995.
XX
PF 14-FEB-1995; 95EP-0200348.
XX
PR 21-DEC-1994; 94EP-0203709.
PR 16-FEB-1994; 94EP-0200337.
XX
PA (ALKU) AKZO NOBEL NV.
XX
PI Adema GT, Fijdor CG;
XX
DR WPI, 1995-284790/38.
DR N-PSDB; AAQ96055.
XX
PT Melanoma associated antigen gp100 - used in vaccines and for the
PT detection of tumours

XX Claim 5; Page 31; 40pp; English.
PS
XX
XX Immunogenic peptides derived from the melanoma associated antigen
CC (see AAR78639-45) may be used in the production of vaccines.
CC Nucleotide sequences encoding the immunogenic peptides may be used
CC as primers and probes in the detection of melanoma cells. Tumour
CC infiltrating lymphocytes capable of binding to the melanoma
CC associated antigen can be cultured ex vivo and returned to melanoma
CC particles, and when radiolabelled, they may be used to identify
CC tumour deposits.
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 59; DB 16; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTWGQYWCY 9
| | | | | | | | | |
DB 3 KTWGQYWCY 11

RESULT 30
AAB61647
ID AAB61647 standard; peptide; 30 AA.
XX
AC AAB61647;
XX
DT 09-APR-2001 (first entry)
XX
DE Gp100 peptide #1.
XX
KW Immunostimulant; vaccine; immune response; parathyroid hormone; antibody;
KW Gp100; melanoma.
XX
OS Unidentified.
XX
PN GB2351905-A.
XX
PD 17-JAN-2001.
XX
PF 13-APR-2000; 2000GB-0008992.
XX
PR 13-APR-1999; 99GB-0008263.
XX
PA (BIND-) BINDING SITE LTD.
XX
PI Bradwell AR, Mead GP;
XX
DR WPI, 2001-140512/15.
XX
PT New antigenic compositions for eliciting improved immune responses,
PT especially in overcoming tolerance to self-antigens -
XX
PS Disclosure; Page 18; 40pp; English.
XX
CC The present invention relates to a composition for eliciting an immune
CC response to a target molecule comprising an immunological adjuvant and
CC one or more peptides. The present sequence is one such peptide. The
CC peptides are similar to, but different from, a target peptide e.g.
CC Gp100. Gp100 is a protein associated with melanoma. The present peptide
CC can elicit the production of antibodies against Gp100, and so can be
CC used to treat melanoma.
XX
SQ Sequence 30 AA;

Query Match 100.0%; Score 59; DB 22; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTWGOXYWQV 9
| | | | | | | |
Db 21 ktwgqywgq 29

Search completed: July 3, 2001, 10:23:58
job time: 1383 sec

7

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OM protein - protein search, using sw_{model}

Run on: July 3, 2001, 10:23:12 ; Search time 23.85 seconds
(without alignments)
28.745 Million cell updates/sec

Title: US-09-214-836-9
Perfect score: 59
Sequence: 1 KTWGQYMOV 9

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR:68:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	662	2	138400 melanoma-associate
2	59	100.0	668	2	441234 melanocyte-specific
3	55	93.2	626	2	S53871 Pmel 17 protein -
4	45	76.3	264	2	H85861 hypothetical prote
5	45	76.3	335	1	A39862 protein-tyrosine-p
6	45	76.3	549	2	H64982 hypothetical prote
7	43	72.9	209	2	S75029 hypothetical prote
8	41	69.5	277	1	ORECST sulfate/chitosulat
9	41	69.5	277	2	H85885 hypothetical prote
10	41	69.5	315	2	T07314 cytochrome c-type
11	40	67.8	281	2	A82104 conserved hypothet
12	40	67.8	305	1	S52775 hypothetical prote
13	40	67.8	400	2	S76446 hypothetical prote
14	40	67.8	807	2	F64844 yods protein precu
15	40	67.8	807	2	F85647 probable outer mem
16	39	66.1	208	2	S46301 fucosanthin chloro
17	39	66.1	236	2	A75530 cytochrome c-type
18	39	66.1	276	2	A72451 probable lactose t
19	39	66.1	794	2	S73378 probable lipoprote
20	38	64.4	160	2	T09871 expansin - upland
21	38	64.4	232	2	T09818 expansin (clone pp
22	38	64.4	232	2	T09821 expansin (clone pp
23	38	64.4	232	2	T09825 expansin (clone pp
24	38	64.4	232	2	T09826 expansin (clone pp
25	38	64.4	237	2	T50654 expansin Exp1 (imp
26	38	64.4	246	2	T04175 expansin - rice
27	38	64.4	246	2	C84444 probable expansin
28	38	64.4	250	2	T10079 expansin S1 precu
29	38	64.4	251	2	T03298 expansin 2 - rice

30	38	64.4	253	2	F84831 probable expansin
31	38	64.4	255	2	T06573 expansin 18 - toma
32	38	64.4	255	2	T50655 expansin EXP5 (imp
33	38	64.4	255	2	T50656 expansin EXP2 (imp
34	38	64.4	257	2	T02727 probable expansin
35	38	64.4	257	2	D84820 probable expansin
36	38	64.4	257	2	T50658 expansin 9 (import
37	38	64.4	258	2	T09786 expansin - upland
38	38	64.4	258	2	S53082 pollen allergen ho
39	38	64.4	258	2	T48247 expansin-like prot
40	38	64.4	259	2	T50653 expansin Exp6 (imp
41	38	64.4	260	2	T08016 probable expansin
42	38	64.4	260	2	T47689 expansin-like prot
43	38	64.4	261	2	T07630 expansin 1 - tomat
44	38	64.4	262	2	T02530 probable expansin
45	38	64.4	262	2	T50660 alpha-expansin 2 (

ALIGNMENTS

RESULT 1
138400 melanoma-associated ME20 antigen (me20m) - human
N:Alternate names: melanoma antigen 25
C:Species: Homo sapiens (man)
C:Date: 01-Nov-1996 #sequence, revision 01-Nov-1996 #text, change 01-Dec-2000
C:Accession: 138400; A53668; A55753
R:Marsh, G.A.; Marken, J.S.; Neubauer, M.; Aruffo, A.; Hellstrom, I.; Hellstrom, K.;
DNA Cell Biol. 13, 87-95, 1994
A:Title: Cloning and expression of the gene for the Melanoma-Associated ME20 Antigen.
A:Reference number: 138400; MUID:94235165
A:Accession: 138400
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-662 <RES>
A:Cross-references: EMBL:U01874; NID:9494939; PIDN:AA18479.1; PID:9494940
R:Adema, G.J.; de Boer, A.J.; Vogel, A.M.; Loenen, W.A.M.; Figdor, C.G.
J. Biol. Chem. 269, 20126-20133, 1994
A:Title: Molecular characterization of the melanocyte lineage-specific antigen gp100.
A:Reference number: A53668; MUID:94327568
A:Accession: A53668
A:Molecule type: mRNA
A:Residues: 1-592,594-662 <ADE>
A:Cross-references: GB:S73003; NID:9639589; PIDN:AAC60634.1; PID:9639580
R:Kawakami, Y.; Eliyahu, S.; Delgado, C.H.; Robbins, P.F.; Sakaguchi, K.; Appella, E.
Proc. Natl. Acad. Sci. U.S.A. 91, 6458-6462, 1994
A:Title: Identification of a human melanoma antigen recognized by tumor-infiltrating
A:Reference number: A55753; MUID:94294401
A:Accession: A55753
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-161, 'F', 163-592,594-662 <KAW>
C:Keywords: glycoprotein

Query Match 100.0%; Score 59; DB 2; Length 662;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KTWGQYMOV 9
|||||||
DB 154 KTWGQYMOV 162

RESULT 2
A41234 melanocyte-specific protein Pmel-17 precursor - human
C:Species: Homo sapiens (man)
C:Date: 19-Jun-1992 #sequence, revision 19-Jun-1992 #text, change 30-Sep-1993
C:Accession: A41234
R:Kwon, B.S.; Chintamaneni, C.; Kozak, C.A.; Copeland, N.G.; Gilbert, D.J.; Jenkins,
Proc. Natl. Acad. Sci. U.S.A. 88, 9228-9232, 1991

A:Title: A melanocyte-specific gene, Pmel 17, maps near the silver coat color locus on H
A:Reference number: A41234; MUID:92021023
A:Accession: A41234
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-668 <KMO>
A:Cross-references: GB:M77348

Query Match
Best Local Similarity 100.0%; Score 59; DB 2; Length 668;
Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KTWGQYMOV 9
|||||
DB 154 KTWGQYMOV 162

RESULT 3
S53871
Pmel 17 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 05-Nov-1999
C:Accession: S53871
R:Kwon, B.S.; Halaban, R.; Ponnazhagan, S.; Kim, K.; Chintamani, C.; Bennett, D.; Pick
Nucleic Acids Res. 23, 134-138, 1995
A:Title: Mouse silver mutation is caused by a single base insertion in the putative cyto
A:Reference number: S53871; MUID:95175358
A:Accession: S53871
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-626 <KMO>
A:Cross-references: GB:U14133; NID:9887940; PIDN:AAA69538.1; PID:9887941

Query Match
Best Local Similarity 93.2%; Score 55; DB 2; Length 626;
Pred. No. 0.47;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KTWGQYMOV 9
|||||
DB 154 KTWGQYMOV 162

RESULT 4
H85861
hypothetical protein 23480 [Imported] - Escherichia coli (strain O157:H7)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C:Accession: H85861
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: H85861
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-264 <STO>
A:Cross-references: GB:AE005174; NID:912516559; PIDN:AA657356.1; GSPDB:GN00145; UMGCP:234
A:Experimental source: strain O157:H7, substrain EDJ933
C:Genetics:
A:Gene: 23480

Query Match
Best Local Similarity 76.3%; Score 45; DB 2; Length 264;
Pred. No. 6.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 WGOYMO 8
|||||
DB 125 WGOYMO 130

RESULT 5
A39862
protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 1 - yeast (Saccharomyces

N:Alternate names: Protein D0815; Protein YDL230w
C:Species: Saccharomyces cerevisiae
C:Date: 30-Dec-1991 #sequence_revision 08-Mar-1996 #text_change 21-Jul-2000
C:Accession: A39862; S67793
R:Guan, K.; Deschenes, R.J.; Qiu, H.; Dixon, J.E.
J. Biol. Chem. 266, 12964-12970, 1991
A:Title: Cloning and expression of a yeast protein tyrosine phosphatase.
A:Reference number: A39862; MUID:91302512
A:Accession: A39862
A:Molecule type: DNA
A:Residues: 1-335 <GUA>
A:Cross-references: GB:M64062; NID:9172295; PIDN:AAA34923.1; PID:9172296
R:Rasmussen, S.W.
submitted to the Protein Sequence Database, July 1996

A:Reference number: S67778
A:Accession: S67793
A:Molecule type: DNA
A:Residues: 1-335 <RAS>
A:Cross-references: EMBL:Z74278; NID:91431387; PIDN:CAA98809.1; PID:91431388; GSPDB:G
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:PTP1; MIPS:YDL230w
A:Cross-references: SGD:S0002389; MIPS:YDL230w
A:Map position: 4L
C:Superfamily: Saccharomyces protein-tyrosine-phosphatase, nonreceptor type 1; protei
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphat
F:52-303/Domain: protein-tyrosine-phosphatase homology <PTP>
F:252/Active site: Cys (phosphocysteine intermediate) #status predicted
F:258/Binding site: substrate phosphate (Arg) #status predicted

Query Match
Best Local Similarity 76.3%; Score 45; DB 1; Length 335;
Pred. No. 8.4;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYMOV 9
|||||
DB 108 KTWGQYMOV 116

RESULT 6
H64992
hypothetical protein b2226 - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 04-Mar-2000
C:Accession: H64992
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: H64992
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-549 <BLAT>
A:Cross-references: GB:AE000312; GB:U00096; NID:91788555; PIDN:AA675286.1; PID:917885
A:Experimental source: strain K-12, substrain MG1655
C:Superfamily: Escherichia coli hypothetical protein b2226

Query Match
Best Local Similarity 76.3%; Score 45; DB 2; Length 549;
Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 WGOYMO 8
|||||
DB 125 WGOYMO 130

RESULT 7
S75029
hypothetical protein slr2003 - *Synechocystis* sp. (strain PCC 6803)
C:Species: *Synechocystis* sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C:Accession: S75029
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
5.
A:Reference number: S74322; MUID:97061201
A:Accession: S75029
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-209 <K&N>
A:Cross-references: EMBL:DB90910; GB:AB001339; NID:q1652956; PIDN:BAAL7891.1; PID:q165297
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: *Synechocystis* hypothetical protein slr2003

Query Match 72.9%; Score 43; DB 2; Length 209;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Oy 1 KTWGOYWO 8
Db 75 KTWGOYWO 82

RESULT 8
ORECST
sulfate/thiosulfate transport protein cyst - *Escherichia coli*
N:Alternate names: sulfate transport system permease protein cyst
C:Species: *Escherichia coli*
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999
C:Accession: A35402; G65016; B35403
R:Sirko, A.; Hryliewicz, M.; Hulanicka, D.; Boeck, A.
J. Bacteriol. 172, 3351-3357, 1990
A:Title: Sulfate and thiosulfate transport in *Escherichia coli* K-12: nucleotide sequence
A:Reference number: A35402; MUID:90264334
A:Accession: A35402
A:Molecule type: DNA
A:Residues: 1-277 <STR>
A:Cross-references: GB:M32101; GB:M38050; NID:q145657; PIDN:AAA23637.1; PID:q145659
A:Experimental source: strain K12
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of *Escherichia coli* K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: G65016
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Accession: G65016
A:Molecule type: DNA
A:Residues: 1-277 <BLAT>
A:Cross-references: GB:AE000330; GB:U00096; NID:q1788763; PIDN:AACT5477.1; PID:q1788764;
A:Experimental source: strain K-12, substrain MG1655
R:Hryliewicz, M.; Sirko, A.; Paluch, A.; Boeck, A.; Hulanicka, D.
J. Bacteriol. 172, 3358-3366, 1990
A:Title: Sulfate and thiosulfate transport in *Escherichia coli* K-12: identification of a
A:Reference number: A35403; MUID:90264335
A:Accession: B35403
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-126; F, 128-133 <HR>
C:Comment: This is one of the membrane-associated components of the binding protein-depe
C:Genetics:
A:Gene: *cytS*; *cytS*
A:Map position: 52 min
C:Superfamily: maltose transport protein malG
C:Keywords: binding protein-dependent transport system; inner membrane; membrane protein

Query Match 69.5%; Score 41; DB 1; Length 277;
Best Local Similarity 62.5%; Pred. No. 28;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Oy 2 TWGOYWOV 9
Db 43 SMOATWEV 50

RESULT 9
B85885
hypothetical protein *cytS* [imported] - *Escherichia coli* (strain O157:H7)
C:Species: *Escherichia coli*
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C:Accession: B85885
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Diallanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
A:Reference number: A83480; MUID:21074935; PMID:11206531
A:Accession: B85885
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-277 <STO>
A:Cross-references: GB:AE005174; NID:q12516799; PIDN:AA657542.1; GSPDB:GN00145; UMGF:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: *cytS*
C:Superfamily: maltose transport protein malG

Query Match 69.5%; Score 41; DB 2; Length 277;
Best Local Similarity 62.5%; Pred. No. 28;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Oy 2 TWGOYWOV 9
Db 43 SMOATWEV 50

RESULT 10
T07314
cytochrome c-type synthesis protein homolog - *Chlorella vulgaris* chloroplast
C:Species: chloroplast *Chlorella vulgaris*
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C:Accession: T07314
R:Wakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Tsudzuki, J.; Na
Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997
A:Title: Complete nucleotide sequence of the chloroplast genome from the green alga C
A:Reference number: Z15985; MUID:97303241
A:Accession: T07314
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-315 <WAK>
A:Cross-references: EMBL:AB001684; NID:q2224352; PIDN:BA57962.1; PID:q2224478
C:Genetics:
A:Gene: *ycf5*
A:Superfamily: cytochrome c-type synthesis protein
C:Keywords: chloroplast

Query Match 69.5%; Score 41; DB 2; Length 315;
Best Local Similarity 71.4%; Pred. No. 31;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KTWGOYWO 7
Db 243 ETWGNW 249

RESULT 11

A82104
conserved hypothetical protein VC2229 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)
C:Species: *Vibrio cholerae*
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: A82104
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Esmolaeva, M.D.; Yamathayan, J.; Bass, S.; Qin, H.; Dragoli, I.; Sellers, F. I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A:Reference number: A82035; MUID:2040933
A:Accession: A82104
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-281 <HEI>
A:Cross-references: GB:AE004294; GB:AE003852; NID:9656774; PIDN:NAF95373.1; GSPDB:GN001
C:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC2229
A:Map position: 1
C:Superfamily: hypothetical protein H11037

Query Match 67.8%; Score 40; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 WGOYW 7
|||||
DB 99 WGOYW 103

RESULT 12
S52775
hypothetical protein 2 - *Chloroflexus aurantiacus*
C:Species: *Chloroflexus aurantiacus*
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: S52775
R:Niedermeier, G.; Shiozawa, J.A.; Lottspeich, F.; Feick, R.G.
FEBS Lett. 342, 61-65, 1994
A:Title: The primary structure of two chlorosome proteins from *Chloroflexus aurantiacus*.
A:Reference number: S43678; MUID:94192803
A:Accession: S52775
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-305 <NIB>
A:Cross-references: EMBL:Z34000; NID:9496485; PIDN:CA83969.1; PID:9496488
A:Note: only a part of the coding sequence is given in this paper
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1994
C:Superfamily: Methanococcus jannaschii conserved hypothetical protein M0279

Query Match 67.8%; Score 40; DB 1; Length 305;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 WGOYW 7
|||||
DB 246 WGOYW 250

RESULT 13
S76446
hypothetical protein - *Synechocystis* sp. (strain PCC 6803)
C:Species: *Synechocystis* sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C:Accession: S76446
R:Kameko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
sp.

A:Reference number: S74322; MUID:97061201
A:Accession: S76446
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-400 <KAN>
A:Cross-references: EMBL:D90915; GB:AB001339; NID:91653604; PIDN:BA18575.1; PID:d101
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 67.8%; Score 40; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 WGOYW 7
|||||
DB 335 WGOYW 339

RESULT 14
F64844
ycds protein precursor - *Escherichia coli*
C:Species: *Escherichia coli*
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 04-Mar-2000
C:Accession: F64844
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of *Escherichia coli* K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: F64844
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-807 <BLAT>
A:Cross-references: GB:AE000204; GB:U00096; NID:91787256; PIDN:ANCA74109.1; PID:917872
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: ycds
C:Superfamily: *Escherichia coli* ycds protein
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-807/Product: ycds protein #status predicted <MAT>

Query Match 67.8%; Score 40; DB 2; Length 807;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 WGOYW 7
|||||
DB 314 WGOYW 318

RESULT 15
F85647
probable outer membrane protein ycds [imported] - *Escherichia coli* (strain O157:H7)
C:Species: *Escherichia coli*
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C:Accession: F85647
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: F85647
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-807 <STO>
A:Cross-references: GB:AE005174; NID:912514389; PIDN:AG55642.1; GSPDB:GN00145; UWGP:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: ycds
C:Superfamily: *Escherichia coli* ycds protein

Query Match 67.8%; Score 40; DB 2; Length 807;
Best Local Similarity 100.0%; Pred. No. 1;le+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 WGOYV 7
|||||
Db 314 WGOYV 318

RESULT 16
S46301

fucocanthin chlorophyll a/c-binding light-harvesting protein - Isochrysis galbana
N:Alternate names: RCP protein

C:Species: Isochrysis galbana

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Nov-1999

C:Accession: S46301

R:LaRoche, J.; Henry, D.; Wyman, K.; Sukenik, A.; Falkowski, P.

Plant Mol. Biol. 25, 355-368, 1994

A:Title: Cloning and nucleotide sequence of a cDNA encoding a major fucocanthin-, chlorophyll family.

A:Reference number: S46301; MUID:94325461

A:Accession: S46301

A:Molecule type: mRNA

A:Residues: 1-208 <IAR>

A:Cross-references: EMBL:X77333; NID:9535080; PIDN:CA54547.1; PID:9535081

A:Experimental source: cultivar DUN

C:Keywords: light-harvesting complex

Query Match 66.1%; Score 39; DB 2; Length 208;
Best Local Similarity 83.3%; Pred. No. 42;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TWGOYV 7
|||||
Db 198 TWGOYV 203

RESULT 17
A75530

cytochrome c-type biogenesis protein, heme exporter protein C - Deinococcus radiodurans

C:Species: Deinococcus radiodurans

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000

C:Accession: A75530

R:White, O.; Eisen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896

A:Accession: A75530

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-236 <WHI>

A:Cross-references: GB:AE001895; GB:AE000513; NID:96458024; PIDN:AF09930.1; PID:9645802

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR0348

A:Map position: 1

C:Superfamily: helc protein

Query Match 66.1%; Score 39; DB 2; Length 236;
Best Local Similarity 83.3%; Pred. No. 48;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TWGOYV 7
|||||
Db 101 TWGOYV 106

RESULT 18
A72451

probable lactose transport system permease protein APE2253 - Aeropyrum pernix (strain
C:Species: Aeropyrum pernix
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C:Accession: A72451
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Ta
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.

DNA Res. 6, 83-101, 1999

A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero

A:Reference number: A72450; MUID:99310339

A:Accession: A72451

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-276 <KAW>

A:Cross-references: DDBJ:AP000064; NID:95105945; PIDN:BA81265.1; PID:95105954

A:Experimental source: strain K1

C:Genetics:

A:Gene: APE2253

C:Superfamily: inner membrane protein upga

Query Match 66.1%; Score 39; DB 2; Length 276;
Best Local Similarity 55.6%; Pred. No. 55;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 KTWGOYMOV 9
|||||
Db 215 KTWGOYMSL 223

RESULT 19
S73328

probable lipoprotein E07.orf794 - Mycoplasma pneumoniae (strain ATCC 29342)

N:Alternate names: MG260 homolog E07.orf794

C:Species: Mycoplasma pneumoniae

A:Variety: ATCC 29342

C>Date: 26-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 07-Dec-1999

C:Accession: S73328

R:Himmelfreich, R.; Hilbert, H.; Piagens, H.; Plöckl, E.; Li, B.C.; Hermann, R.

Nucleic Acids Res. 24, 4420-4449, 1996

A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumon

A:Reference number: S73327; MUID:97105885

A:Accession: S73328

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-794 <HIM>

A:Cross-references: EMBL:AE000001; GB:U00089; NID:91673645; PIDN:AB95650.1; PID:9167

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996

C:Genetics:

A:Genetic code: SGC3

C:Superfamily: hypothetical protein MG185

Query Match 66.1%; Score 39; DB 2; Length 794;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGOYMOV 9
|||||
Db 268 KTWGOYDEV 276

RESULT 20
T09871

expansin - upland cotton (fragment)

C:Species: Gossypium hirsutum (upland cotton)

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C:Accession: T09871

R:Shimizu, Y.; Aotsuka, S.; Hasegawa, O.; Kawada, T.; Sakuno, T.; Sakai, F.; Hayashi,

Plant Cell Physiol. 38, 373-376, 1997

A:Title: Changes in levels of mRNAs for cell wall-related enzymes in growing cotton f

A:Reference number: Z16889; MUID:97294938

A:Accession: T09871

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA
A:Residues: 1-160 <SH1>
A:Cross-references: EMBL:D88415; NID:g2244735; PIDN:BAA21109.1; PID:g2244736
A:Experimental source: strain Coker12; fiber
C:Superfamily: expansin

Query Match 64.4%; Score 38; DB 2; Length 160;
Best Local Similarity 62.5%; Pred. No. 47;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 KTWGQYWO 8
DB 110 RNMGQNMW 117

RESULT 21
T09818
expansin (clone ptxexp2) - 10b101ly pine (fragment)
C:Species: Pinus taeda (10b101ly pine)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
C:Accession: T09818
R:Hutchinson, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S.
submitted to the EMBL Data Library, July 1996
A:Description: Expansins are conserved in conifers and expressed in response to exogenous
A:Reference number: Z16866
A:Accession: T09818
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-232 <HUT>
A:Cross-references: EMBL:U64890; NID:g1778098; PID:g1778099
A:Experimental source: clone ptxexp2; hypocotyl
C:Superfamily: expansin

Query Match 64.4%; Score 38; DB 2; Length 232;
Best Local Similarity 62.5%; Pred. No. 67;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 KTWGQYWO 8
DB 182 RNMGQNMW 189

RESULT 22
T09821
expansin (clone ptxexp3) - 10b101ly pine (fragment)
C:Species: Pinus taeda (10b101ly pine)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
C:Accession: T09821
R:Hutchinson, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S.
submitted to the EMBL Data Library, July 1996
A:Description: Expansins are conserved in conifers and expressed in response to exogenous
A:Reference number: Z16866
A:Accession: T09821
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-232 <HUT>
A:Cross-references: EMBL:U64891; NID:g1778100; PID:g1778101
A:Experimental source: clone ptxexp3
C:Superfamily: expansin

Query Match 64.4%; Score 38; DB 2; Length 232;
Best Local Similarity 62.5%; Pred. No. 67;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 KTWGQYWO 8
DB 182 RNMGQNMW 189

RESULT 23

T09825
expansin (clone ptxexp4) - 10b101ly pine (fragment)
C:Species: Pinus taeda (10b101ly pine)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
C:Accession: T09825
R:Hutchinson, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S.
submitted to the EMBL Data Library, July 1996
A:Description: Expansins are conserved in conifers and expressed in response to exogenous
A:Reference number: Z16866
A:Accession: T09825
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-232 <HUT>
A:Cross-references: EMBL:U64892; NID:g1778102; PID:g1778103
A:Experimental source: clone ptxexp4
C:Superfamily: expansin

Query Match 64.4%; Score 38; DB 2; Length 232;
Best Local Similarity 62.5%; Pred. No. 67;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 KTWGQYWO 8
DB 182 RNMGQNMW 189

RESULT 24
T09826
expansin (clone ptxexp5) - 10b101ly pine (fragment)
C:Species: Pinus taeda (10b101ly pine)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
C:Accession: T09826
R:Hutchinson, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S.
submitted to the EMBL Data Library, July 1996
A:Description: Expansins are conserved in conifers and expressed in response to exogenous
A:Reference number: Z16866
A:Accession: T09826
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-232 <HUT>
A:Cross-references: EMBL:U64893; NID:g1778104; PID:g1778105
A:Experimental source: clone ptxexp5
C:Superfamily: expansin

Query Match 64.4%; Score 38; DB 2; Length 232;
Best Local Similarity 62.5%; Pred. No. 67;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 KTWGQYWO 8
DB 182 RNMGQNMW 189

RESULT 25
T50654
expansin EXP1 [imported] - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 02-Sep-2000
C:Accession: T50654
R:Shcherban, T.Y.; Shi, J.; Durachko, D.M.; Guiltinan, M.J.; McQueen-Mason, S.J.; Shi
Proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995
A:Title: Molecular cloning and sequence analysis of expansins--a highly conserved, mu
A:Reference number: Z14894; MUID:96016146
A:Accession: T50654
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-237 <SHC>
A:Cross-references: EMBL:U30476; PIDN:AAB38070.1
C:Genetics:
A:Gene: EXP1
C:Function:

A:Description: induces extension (creep) in plant cell walls
C:Superfamily: expansin
C:Keywords: cell wall

Query Match 64.4%; Score 38; DB 2; Length 237;
Best Local Similarity 62.5%; Pred. No. 68;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 KTWGQYMQ 8
: ||| ||
Db 186 RNMGQNMQ 193

RESULT 26
T04175
expansin - rice
C:Species: Oryza sativa (rice)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 26-May-2000
C:Accession: T04175
R:Cho, H.T.; Kende, H.
Plant Cell 9, 1661-1671, 1997
A:Title: Expression of expansin genes is correlated with growth in deepwater ce.
A:Reference number: 215042; MUID:97480100
A:Accession: T04175
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-246 <CHO>
A:Cross-references: EMBL:U085246; NID:G1815680; PIDN:AMB81662.1; PID:G1815681
A:Experimental source: cv. Pin Gaew 56
C:Genetics:
A:Gene: EXP4
C:Superfamily: expansin

Query Match 64.4%; Score 38; DB 2; Length 246;
Best Local Similarity 62.5%; Pred. No. 70;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 KTWGQYMQ 8
: ||| ||
Db 196 RNMGQNMQ 203

RESULT 27
C84444
probable expansin [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C:Accession: C84444
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffit, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
Euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: C84444
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-248 <STO>
A:Cross-references: GB:AE002093; NID:G3461833; PIDN:AMC32927.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g03090
A:Map position: 2
C:Superfamily: expansin

Query Match 64.4%; Score 38; DB 2; Length 248;
Best Local Similarity 62.5%; Pred. No. 71;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 KTWGQYMQ 8
: ||| ||

Db 197 RNMGQNMQ 204

RESULT 28
T10079
expansin S1 precursor - cucumber
C:Species: Cucumis sativus (cucumber)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: T10079
R:Shcherban, T.Y.; Shi, J.; Durachko, D.M.; Gultinan, M.J.; McQueen-Mason, S.J.; Shi
Proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995
A:Title: Molecular cloning and sequence analysis of expansins--a highly conserved, mu
A:Reference number: 214894; MUID:96016146
A:Accession: T10079
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-250 <SHC>
A:Cross-references: EMBL:U030382; NID:G1040874; PIDN:AMB37746.1; PID:G1040875
A:Experimental source: cultivar Burpee Pickler
C:Genetics:
A:Gene: EXP1
C:Function:
A:Description: mediates cell wall extension
C:Superfamily: expansin
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-250/Product: expansin #status predicted <MAT>

Query Match 64.4%; Score 38; DB 2; Length 250;
Best Local Similarity 62.5%; Pred. No. 71;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 KTWGQYMQ 8
: ||| ||
Db 200 RNMGQNMQ 207

RESULT 29
T03298
expansin 2 - rice
C:Species: Oryza sativa (rice)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
C:Accession: T03298
R:Shcherban, T.Y.; Shi, J.; Durachko, D.M.; Gultinan, M.J.; McQueen-Mason, S.J.; Shi
Proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995
A:Title: Molecular cloning and sequence analysis of expansins--a highly conserved, mu
A:Reference number: 214894; MUID:96016146
A:Accession: T03298
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-251 <SHC>
A:Cross-references: EMBL:U030477; NID:G1041709; PIDN:AMB8074.1; PID:G1041710
C:Genetics:
A:Gene: EXP2
C:Function:
A:Description: induces extension (creep) in plant cell
C:Superfamily: expansin

Query Match 64.4%; Score 38; DB 2; Length 251;
Best Local Similarity 62.5%; Pred. No. 72;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 KTWGQYMQ 8
: ||| ||
Db 201 RNMGQNMQ 208

RESULT 30
F84831
probable expansin [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001

C:Accession: F84831
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
Evens, D.; Niernan, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, A.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A:Reference number: A84420; MUID:20083487
A:Accession: F84831
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-253 <STO>
A:Cross-references: GB:AE002093; NID:g2651297; PIDN:AAB87577.1; GSPDB:GN00139
C:genetics:
A:gene: Atg40610
A:Map position: 2
C:Superfamily: expansin

Query Match 64.48; Score 38; DB 2; Length 253;
Best Local Similarity 62.58; Pred. No. 72;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 KTWGQYMQ 8
Db 203 RNWGQNNQ 210

Search completed: July 3, 2001, 10:23:12
Job time: 1337 sec

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OM protein - protein search, using sw model

Run on: July 3, 2001, 10:22:35 ; Search time 21.69 Seconds
(without alignments)
8.359 Million cell updates/sec

Title: US-09-214-836-9

Perfect score: 59

Sequence: 1 KTWGQYMOY 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	9	1	US-08-787-547-61
2	59	100.0	9	2	US-08-417-174-46
3	59	100.0	9	2	US-08-902-516-29
4	59	100.0	9	2	US-09-036-582-26
5	59	100.0	10	2	US-08-417-174-47
6	59	100.0	661	2	US-08-417-174-121
7	59	100.0	668	1	US-07-891-9426-6
8	55	93.2	661	2	US-08-417-174-27
9	55	93.2	661	2	US-08-231-565A-27
10	55	93.2	661	2	US-09-007-961-27
11	54	91.5	9	2	US-08-417-174-71
12	54	91.5	9	2	US-08-417-174-72
13	54	91.5	9	2	US-08-417-174-73
14	54	91.5	9	2	US-08-417-174-74
15	54	91.5	9	2	US-08-417-174-75
16	53	89.8	9	2	US-08-417-174-68
17	53	89.8	9	2	US-08-417-174-69
18	53	89.8	9	2	US-08-417-174-70
19	50	84.7	9	2	US-08-417-174-76
20	49	83.1	9	2	US-08-417-174-77
21	49	83.1	9	2	US-08-417-174-78
22	49	83.1	9	2	US-08-417-174-79
23	49	83.1	9	2	US-08-417-174-80
24	49	83.1	9	2	US-08-417-174-81
25	49	83.1	9	2	US-08-417-174-82
26	38	64.4	12	1	US-08-439-817-205
27	38	64.4	20	1	US-08-241-054-85

28	38	64.4	20	1	US-08-241-054-91	Sequence 91, Appl
29	38	64.4	20	1	US-08-390-156A-40	Sequence 40, Appl
30	38	64.4	20	1	US-08-390-156A-43	Sequence 43, Appl
31	38	64.4	20	1	US-08-439-817-65	Sequence 65, Appl
32	38	64.4	20	1	US-08-439-817-71	Sequence 71, Appl
33	38	64.4	20	1	US-08-485-508-85	Sequence 85, Appl
34	38	64.4	20	1	US-08-485-508-91	Sequence 91, Appl
35	38	64.4	72	1	US-08-482-782B-6	Sequence 6, Appl
36	38	64.4	72	1	US-08-486-036A-6	Sequence 6, Appl
37	38	64.4	72	5	PCT-US96-09848-6	Sequence 6, Appl
38	38	64.4	167	2	US-08-845-539-4	Sequence 6, Appl
39	38	64.4	179	2	US-08-845-539-6	Sequence 6, Appl
40	38	64.4	222	2	US-08-440-517A-3	Sequence 3, Appl
41	38	64.4	225	2	US-08-845-539-2	Sequence 2, Appl
42	38	64.4	225	2	US-08-440-517A-5	Sequence 5, Appl
43	38	64.4	226	2	US-08-440-517A-6	Sequence 6, Appl
44	38	64.4	228	2	US-08-440-517A-2	Sequence 2, Appl
45	38	64.4	401	5	PCT-US96-09848-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-08-787-547-61
Sequence 61, Application US/08787547
Patent No. 5783567
GENERAL INFORMATION:
APPLICANT: Hedley, Mary Lynne
APPLICANT: Curley, Joanne M.
APPLICANT: Langer, Robert S.
TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
TITLE OF INVENTION: OF NOCLEIC ACID
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/787,547
FILING DATE: 22-JAN-1997
CLASSIFICATION: 51A
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08191/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-787-547-61
Query Match 100.0%; Score 59; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Caps 0;

OY 1 KTWGOYMOV 9
|111111111|
Db 1 KTWGOYMOV 9

RESULT 2

US-08-417-174-46
; Sequence 46, Application US/08417174
; Patent No. 5844075
; GENERAL INFORMATION:
; APPLICANT: KAKAKAMI, YUTAKA; ROSENBERG,
; APPLICANT: STEVEN A.
; TITLE OF INVENTION: MELANOMA ANTIGENS AND
; THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 126
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/417,174
; FILING DATE: 05-APR-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,565
; FILING DATE: 22-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CAROL M. GRUPTI
; REGISTRATION NUMBER: 37,341
; REFERENCE/DOCKET NUMBER: 2026-4124US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: amino acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-08-417-174-46

Query Match 100.0%; Score 59; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KTWGOYMOV 9
|111111111|
Db 1 KTWGOYMOV 9

RESULT 3
US-08-902-516-29
; Sequence 29, Application US/08902516
; Patent No. 5891432
; GENERAL INFORMATION:
; APPLICANT: SOO HOO, WILLIAM
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
; TITLE OF INVENTION: COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
; TITLE OF INVENTION: RESPONSE USING SAME
; NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL & FLORES, LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92121

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,516
FILING DATE: 29-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IM 2442
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)535-9001
TELEFAX: (619)535-8949
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-902-516-29

Query Match 100.0%; Score 59; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KTWGOYMOV 9
|111111111|
Db 1 KTWGOYMOV 9

RESULT 4
US-09-036-582-26
; Sequence 26, Application US/09036582A
; Patent No. 5965381
; GENERAL INFORMATION:
; APPLICANT: van der Bruggen, Pierre
; TITLE OF INVENTION: DELIVERY OF PROTEINS INTO EUKARYOTIC CELLS.
; FILE REFERENCE: 11154
; CURRENT APPLICATION NUMBER: US/09/036,582A
; CURRENT FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 9
; TYPE: PPT
; ORGANISM: Human gp100Pmel117 peptide
US-09-036-582-26

Query Match 100.0%; Score 59; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KTWGOYMOV 9
|111111111|
Db 1 KTWGOYMOV 9

RESULT 5
US-08-417-174-47

Sequence 47, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6849
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-47

Query Match 100.0%; Score 59; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTWGQYMOV 9
Db 1 KTWGQYMOV 9

RESULT 6
US-08-417-174-121
Sequence 121, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6849
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 661
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Protein
US-08-417-174-121

Query Match 100.0%; Score 59; DB 2; Length 661;
Best Local Similarity 100.0%; Pred. No. 0.097;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTWGQYMOV 9
Db 154 KTWGQYMOV 162

RESULT 7
US-07-891-9426-6
Sequence 6, Application US/07891942G
Patent No. 5679511
GENERAL INFORMATION:
APPLICANT: Kwon, Byoung Se
TITLE OF INVENTION: CDNA CLONES FOR HUMAN TYROSINASE AND FOR
TITLE OF INVENTION: A REGULATORY PROTEIN IN THE MELANIN PROTEIN PATHWAY
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christopher A. Michaels, Barnard, Brown &
STREET: 306 East State Street; Suite 220
CITY: Ithaca
STATE: NY
COUNTRY: USA
ZIP: 14850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,942G
FILING DATE: 01-JUN-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/915,753
FILING DATE: 06-OCT-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/362,847
FILING DATE: 07-JUN-1989
ATTORNEY/AGENT INFORMATION:
NAME: Michaels, Christopher A

REGISTRATION NUMBER: 34,390
REFERENCE/DOCKET NUMBER: INDI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 607-273-1711
TELEFAX: 607-273-2609
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 668 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PUBLICATION INFORMATION:
AUTHORS: Kwon, Byoung Se
AUTHORS: Chintamaneni, Chaya
AUTHORS: Kozak, Christine A
AUTHORS: Copeland, Neal G
AUTHORS: Gilbert, Debra J
AUTHORS: Jenkins, Nancy
AUTHORS: Barton, David
AUTHORS: Francke, Uta
AUTHORS: Kobayashi, Yvonne
AUTHORS: Kim, Kack K
TITLE: A melanocyte-specific gene, Pmel 17, maps
TITLE: near the silver coat color locus on mouse
TITLE: chromosome 10 and is in a syntenic region on human
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
VOLUME: 88
PAGES: 9228-9232
DATE: October-1991
RELEVANT RESIDUES IN SEQ ID NO: 6: FROM 1 TO 668
US-07-891-942G-6

Query Match 100.0%; Score 59; DB 1; Length 668;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTWGQYMW 9
DB 154 KTWGQYMW 162

RESULT 8
US-08-417-174-27
Sequence 27, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 661
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: Protein
US-08-417-174-27

Query Match 93.2%; Score 55; DB 2; Length 661;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTWGQYMW 8
DB 154 KTWGQYMW 161

RESULT 9
US-08-231-565A-27
Sequence 27, Application US/08231565A
Patent No. 5874560
GENERAL INFORMATION:
APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565A
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 661
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: Protein
US-08-231-565A-27

Query Match 93.2%; Score 55; DB 2; Length 661;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTWGQYWO 8
Db 154 KTWGQYWO 161

RESULT 10

US-09-007-961-27
; Sequence 27, Application US/09007961
; Patent No. 5994523

GENERAL INFORMATION:

APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,

APPLICANT: STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND

TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC

TITLE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/007,961

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/231,565

FILING DATE: 22-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI

REGISTRATION NUMBER: 37,341

REFERENCE/DOCKET NUMBER: 2026-4124

TELEPHONE: (212) 758-4800

TELEFAX: (212) 751-6849

TELEX: 421792

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 661

TYPE: amino acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

MOLECULE TYPE: Protein

US-09-007-961-27

Query Match 93.2%; Score 55; DB 2; Length 661;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTWGQYWO 8
Db 154 KTWGQYWO 161

RESULT 11

US-08-417-174-71

; Sequence 71, Application US/08417174

; Patent No. 5844075

GENERAL INFORMATION:

APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,

APPLICANT: STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 126

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/417,174

FILING DATE: 05-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/231,565

FILING DATE: 22-APR-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI

REGISTRATION NUMBER: 37,341

REFERENCE/DOCKET NUMBER: 2026-4124051

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800

TELEFAX: (212) 751-6849

TELEX: 421792

INFORMATION FOR SEQ ID NO: 71:

SEQUENCE CHARACTERISTICS:

LENGTH: 9

TYPE: amino acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

MOLECULE TYPE: Peptide

US-08-417-174-71

Query Match 91.5%; Score 54; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TWGQYWO 9
Db 2 TWGQYWO 9

RESULT 12

US-08-417-174-72

; Sequence 72, Application US/08417174

; Patent No. 5844075

GENERAL INFORMATION:

APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,

APPLICANT: STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND

TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC

TITLE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 126

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/417,174
;; FILING DATE: 05-APR-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/231,565
;; FILING DATE: 22-APR-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: CAROL M. GRUPE
;; REGISTRATION NUMBER: 37,341
;; REFERENCE/DOCKET NUMBER: 2026-4124US1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 758-4800
;; TELEFAX: (212) 751-6849
;; TELEEX: 421792
;; INFORMATION FOR SEQ ID NO: 72:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9
;; TYPE: amino acid
;; STRANDEDNESS: Unknown
;; TOPOLOGY: Unknown
;; MOLECULE TYPE: Peptide
US-08-417-174-72

Query Match 91.5%; Score 54; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TWGQYMOV 9
DB 2 TWGQYMOV 9

RESULT 13
US-08-417-174-73
;; Sequence 73, Application US/08417174
;; Patent No. 5844075
;; GENERAL INFORMATION:
;; APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
;; APPLICANT: STEVEN A.
;; TITLE OF INVENTION: MELANOMA ANTIGENS AND
;; TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
;; NUMBER OF SEQUENCES: 126
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
;; STREET: 345 PARK AVENUE
;; CITY: NEW YORK
;; STATE: NEW YORK
;; COUNTRY: USA
;; ZIP: 10154
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: FLOPPY DISK
;; COMPUTER: IBM PC COMPATIBLE
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: ASCII
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/417,174
;; FILING DATE: 05-APR-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/231,565
;; FILING DATE: 22-APR-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: CAROL M. GRUPE
;; REGISTRATION NUMBER: 37,341
;; REFERENCE/DOCKET NUMBER: 2026-4124US1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 758-4800
;; TELEFAX: (212) 751-6849
;; TELEEX: 421792
;; INFORMATION FOR SEQ ID NO: 73:

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9
;; TYPE: amino acid
;; STRANDEDNESS: Unknown
;; TOPOLOGY: Unknown
;; MOLECULE TYPE: Peptide
US-08-417-174-73

Query Match 91.5%; Score 54; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TWGQYMOV 9
DB 2 TWGQYMOV 9

RESULT 14
US-08-417-174-74
;; Sequence 74, Application US/08417174
;; Patent No. 5844075
;; GENERAL INFORMATION:
;; APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
;; APPLICANT: STEVEN A.
;; TITLE OF INVENTION: MELANOMA ANTIGENS AND
;; TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
;; NUMBER OF SEQUENCES: 126
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
;; STREET: 345 PARK AVENUE
;; CITY: NEW YORK
;; STATE: NEW YORK
;; COUNTRY: USA
;; ZIP: 10154
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: FLOPPY DISK
;; COMPUTER: IBM PC COMPATIBLE
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: ASCII
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/417,174
;; FILING DATE: 05-APR-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/231,565
;; FILING DATE: 22-APR-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: CAROL M. GRUPE
;; REGISTRATION NUMBER: 37,341
;; REFERENCE/DOCKET NUMBER: 2026-4124US1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 758-4800
;; TELEFAX: (212) 751-6849
;; TELEEX: 421792
;; INFORMATION FOR SEQ ID NO: 74:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9
;; TYPE: amino acid
;; STRANDEDNESS: Unknown
;; TOPOLOGY: Unknown
;; MOLECULE TYPE: Peptide
US-08-417-174-74

Query Match 91.5%; Score 54; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TWGQYMOV 9
DB 2 TWGQYMOV 9

RESULT 15
US-08-417-174-75
Sequence 75, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-75

Query Match 91.5%; Score 54; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TWGQYMOV 9
DB 2 TWGQYMOV 9

RESULT 16
US-08-417-174-68
Sequence 68, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE

CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-68

Query Match 89.8%; Score 53; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTWGQYMOV 9
DB 1 KTWGQYMOV 9

RESULT 17
US-08-417-174-69
Sequence 69, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435

Same as
w/09/24/93
240995
Seq No 68

ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-69

Query Match 89.8%; Score 53; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTMGOYMOV 9
1 |||||
Db 1 KMGQYMOV 9

RESULT 18
US-08-417-174-70
Sequence 70, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
NUMBER OF INVENTION: METHODS
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-70

Query Match 89.8%; Score 53; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTMGOYMOV 9
1 |||||
Db 1 KMGQYMOV 9

RESULT 19
US-08-417-174-76
Sequence 76, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
NUMBER OF INVENTION: METHODS
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-76

Query Match 84.7%; Score 50; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KTMGOYMOV 9
1 |||||
Db 1 KMGQYMOV 9

RESULT 20
US-08-417-174-77
Sequence 77, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:

```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6800
TELEFAX: (212) 751-6849
TELEX: 421792
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 78:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-78

Query Match 83.1%; Score 49; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 14e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 3 WGYWQV 9
|||||
Db 3 WGYWQV 9

RESULT 22
US-08-417-79
; Sequence 79, Application US/08417174
; Patent No. 5844075
; GENERAL INFORMATION:
; APPLICANT: KAKAKAMI, YUTAKA; ROSENBERG,
; APPLICANT: STEVEN A.
; TITLE OF INVENTION: MELANOMA ANTIGENS AND
; TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 126
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/417,174
; FILING DATE: 05-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,565
; FILING DATE: 22-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CAROL M. GRUPPI
; REGISTRATION NUMBER: 37,341
; REFERENCE/DOCKET NUMBER: 2026-4124US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 751-6800
; TELEFAX: (212) 751-6849
; TELEX: 421792

```

TELEX: 421792
INFORMATION FOR SEQ ID NO: 79;
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-79

Query Match 83.1%; Score 49; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 WGOYMOV 9
|||||
DB 3 WGOYMOV 9

RESULT 23

US-08-417-174-80
Sequence 80, Application US/08417174
Patent No. 5844075

GENERAL INFORMATION:

APPLICANT: KAKAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC

TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC

NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/417,174

FILING DATE: 05-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/231,565

FILING DATE: 22-APR-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI

REGISTRATION NUMBER: 37,341

REFERENCE/DOCKET NUMBER: 2026-4124US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 751-6849

TELEFAX: (212) 758-4800

TELEX: 421792

INFORMATION FOR SEQ ID NO: 80:

SEQUENCE CHARACTERISTICS:

LENGTH: 9

TYPE: amino acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

MOLECULE TYPE: Peptide

US-08-417-174-80

Query Match 83.1%; Score 49; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 WGOYMOV 9

DB 3 WGOYMOV 9
|||||

RESULT 24

US-08-417-174-81

Sequence 81, Application US/08417174

Patent No. 5844075

GENERAL INFORMATION:

APPLICANT: KAKAKAMI, YUTAKA; ROSENBERG,

APPLICANT: STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND

THEIR USE IN DIAGNOSTIC AND THERAPEUTIC

TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC

NUMBER OF SEQUENCES: 126

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/417,174

FILING DATE: 05-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/231,565

FILING DATE: 22-APR-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI

REGISTRATION NUMBER: 37,341

REFERENCE/DOCKET NUMBER: 2026-4124US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 751-6849

TELEFAX: (212) 758-4800

TELEX: 421792

INFORMATION FOR SEQ ID NO: 81:

SEQUENCE CHARACTERISTICS:

LENGTH: 9

TYPE: amino acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

MOLECULE TYPE: Peptide

US-08-417-174-81

Query Match 83.1%; Score 49; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 WGOYMOV 9
|||||
DB 3 WGOYMOV 9

RESULT 25

US-08-417-174-82

Sequence 82, Application US/08417174

Patent No. 5844075

GENERAL INFORMATION:

APPLICANT: KAKAKAMI, YUTAKA; ROSENBERG,

APPLICANT: STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND

THEIR USE IN DIAGNOSTIC AND THERAPEUTIC

TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC

NUMBER OF SEQUENCES: 126

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION NUMBER: US/08/417,174
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-82

Query Match 83.1%; Score 49; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 WGOYMOV 9
|||||
Db 3 WGOYMOV 9

RESULT 26
US-08-439-817-205
Sequence 205, Application US/08439817
Patent No. 5728802
GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwiria, Steven E.
APPLICANT: Dower, William J.
APPLICANT: Koller, Kerry J.
APPLICANT: Lee, Jung
APPLICANT: Martens, Christine L.
APPLICANT: Ruhland-Fritsch, Beatrice
TITLE OF INVENTION: Peptides and Compounds That Bind
TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
TITLE OF INVENTION: Molecule I (ELAM-1)
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies, NV
STREET: 4001 Miranda Ave.
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,817
FILING DATE: 12-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/241,054
FILING DATE: 11-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 000324-046/1056.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 205:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-439-817-205

Query Match 64.4%; Score 38; DB 1; Length 12;
Best Local Similarity 62.5%; Pred. No. 2.6;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 TWGQYMOV 9
|||||
Db 3 TWGQYMOV 10

RESULT 27
US-08-241-054-85
Sequence 85, Application US/08241054
Patent No. 5643873
GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwiria, Steven E.
APPLICANT: Dower, William J.
APPLICANT: Koller, Kerry J.
APPLICANT: Lee, Jung
APPLICANT: Martens, Christine L.
APPLICANT: Ruhland-Fritsch, Beatrice
TITLE OF INVENTION: Peptides and Compounds That Bind
TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
TITLE OF INVENTION: Molecule 1
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22313
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241,054
FILING DATE: 11-MAY-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295

FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gerald F. Swiss
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 000324-002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
INFORMATION FOR SEQ. ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-241-054-85

Query Match 64.4%; Score 38; DB 1; Length 20;
Best Local Similarity 62.5%; Pred. No. 4.3;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TWGQYMOV 9
DB 7 TWGQWMDL 14

RESULT 28
US-08-241-054-91
Sequence 91, Application US/08241054
Patent No. 5643873
GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Dower, William J.
APPLICANT: Koller, Kerry J.
APPLICANT: Lee, Jung
APPLICANT: Martens, Christine L.
APPLICANT: Rubland-Fritsch, Beatrice
TITLE OF INVENTION: Peptides and Compounds That Bind
TITLE OF INVENTION: Selectins Including Endothelium Leukocyte Adhesion
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22313
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241,054
FILING DATE: 11-MAY-1994
CLASSIFICATION: 350
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gerald F. Swiss
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 000324-002
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
INFORMATION FOR SEQ. ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-241-054-91

Query Match 64.4%; Score 38; DB 1; Length 20;
Best Local Similarity 62.5%; Pred. No. 4.3;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TWGQYMOV 9
DB 7 TWGQWMDL 14

RESULT 29
US-08-390-156A-40
Sequence 40, Application US/08390156A
Patent No. 5648458
GENERAL INFORMATION:
APPLICANT: Cwirla, Steven E.
APPLICANT: Barrett, Ronald W.
APPLICANT: Dower, William J.
APPLICANT: Martens, Christine L.
TITLE OF INVENTION: Peptides and Compounds That Bind to
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies, N.V.
STREET: 4001 Miranda Ave.
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,156A
FILING DATE: 16-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 1023.1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ. ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-390-156A-40

Query Match 64.4%; Score 38; DB 1; Length 20;
Best Local Similarity 62.5%; Pred. No. 4.3;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 TWGQYMOV 9

Db 7 TWGQIMDL 14

RESULT 30

US-08-390-156A-43

; Sequence 43; Application US/08390156A

; Patent No. 5648458

; GENERAL INFORMATION:

; APPLICANT: Cwitra, Steven E.

; APPLICANT: Barrett, Ronald W.

; APPLICANT: Dower, William J.

; APPLICANT: Martens, Christine L.

; TITLE OF INVENTION: Peptides and Compounds That Bind to

; TITLE OF INVENTION: EIAM-1

; NUMBER OF SEQUENCES: 113

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Affymax Technologies, N.V.

; STREET: 4001 Miranda Ave.

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/390,156A

; FILING DATE: 16-FEB-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/057,295

; FILING DATE: 05-MAY-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/881,395

; FILING DATE: 06-MAY-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Swiss, Gerald F.

; REGISTRATION NUMBER: 30,113

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-424-0832

; TELEFAX: 415-424-0832

; INFORMATION FOR SEQ ID NO: 43:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 20 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-390-156A-43

Query Match 64.4%; Score 38; DB 1; Length 20;

Best Local Similarity 62.5%; Pred. No. 4.3;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 TWGQYMOV 9

Db 7 TWGQIMDL 14

Search completed: July 3, 2001, 10:22:35
Job time: 1300 sec

